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STIC-Biotech/ChemLib

From: Elliott, George
Sent: Tuesday, March 14, 2000 8:47 AM
To: STIC-Biotech/ChemLib
Cc: Hamud, Fozia
Subject: FW: rush search 09/167,705

Please rush.

Thanks,

George

-----Original Message-----

From: Hamud, Fozia
Sent: Tuesday, March 14, 2000 8:17 AM
To: Elliott, George
Subject: rush search 09/167,705

Good morning Mr. Elliot, 09/167,705 is an amended case due this Bi-week. I would like to request rush search. Thanks. Please search SEQ ID NO:s 1 and 2 against commercial data bases and please conduct interference search for both sequences. Thanks.

Fozia Hamud
Art Unit 1646
Crystal-Mall-One, Room 10D06
308-8896

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2000, 15:45:53 ; Search time 216.93 Seconds
(without alignments)
-5478.334 Million cell updates/sec

Title: US-09-167-705-1

Perfect score: 395
Sequence: 1 atgactaagtgtgagaccca.....agcaaaaaaaaaaaaaa 395

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 821193 seqs, -1518192014 residues
tal number of hits satisfying chosen parameters: 1642386

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_om: *
4: gb_ov: *
5: gb_pat: *
6: gb_ph: *
7: gb_pl1: *
8: gb_pl2: *
9: gb_pl3: *
10: gb_pl4: *
11: gb_pl5: *
12: gb_pl6: *
13: gb_pl7: *
14: gb_pl8: *
15: gb_pl9: *
16: gb_pl10: *
17: gb_pl11: *
18: gb_pl12: *
19: gb_pl13: *
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21: gb_pl15: *
22: gb_pl16: *
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25: gb_pl19: *
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37: gb_pl31: *
38: gb_pl32: *
39: gb_pl33: *
40: gb_pl34: *
41: gb_pl35: *
42: gb_pl36: *
43: gb_pl37: *
44: gb_pl38: *

45: gb_htg7: *
46: em_htg1: *
47: em_htg2: *
48: em_htg3: *
49: em_hum5: *
50: gb_pl13: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	319.2	80.8	405	10	AF011757
2	304	77.0	429	3	D49548 Bos taurus
3	304	77.0	429	24	E12013 cDNA encodi
4	304	77.0	429	24	E12020 cDNA encodi
5	164.4	41.6	441	24	E12012 cDNA encodi
6	164.4	41.6	442	9	D49549 Homo sapien
7	164.4	41.6	461	9	HSCALGRAN
8	164.4	41.6	466	9	D83664 Human mRNA
9	129.2	32.7	355	3	AF091848 Oryctolag
10	87.2	22.1	598	4	G6126MRP
11	86	21.8	532	9	HSS1002
12	86	21.8	4992	9	D83657
13	86	21.8	111213	45	AC011666
14	83.6	21.2	480	3	AF091849
15	81	20.5	287	9	HSS1003
16	75.6	19.1	336	5	A12024
17	75.6	19.1	462	5	A12029
18	75.6	19.1	462	5	HSMP14
19	75.6	19.1	565	10	HMCFA
20	75.6	19.1	567	11	HUM2D66A09
21	75.6	19.1	571	5	AR015928
22	69.6	17.6	1488	12	RATSI00B
23	69.6	17.6	1488	12	RATSI00P
24	69.6	17.5	538	4	AF077613
25	65.4	16.6	488	3	D89056
26	64.8	16.4	273	13	G24223
27	63.8	16.2	283	14	SYNS100SYN
28	63.4	16.1	439	9	HSS100PCB
29	61.4	15.5	284	5	A12022
30	61.4	15.5	408	5	AR015927
31	61.4	15.5	418	9	HSMP8
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33	61.4	15.5	485	5	A12025
34	61.2	15.5	286	12	RMP9K42AB
35	61.2	15.5	487	12	RATSI00RO
36	59.6	15.1	455	12	KMCBPR
37	59.6	15.1	503	12	MOSPEL98
38	59.6	15.1	744	12	MRMTSIGAG
39	59.4	15.0	506	12	AF087687
40	59	14.9	264	12	RATSI00BS
41	59	14.9	303	5	AR025425
42	59	14.9	303	5	AR037321
43	59	14.9	303	5	AR062122
44	58.8	14.9	2737	5	A12031
45	58.8	14.9	4439	9	HUMMRP14A

ALIGNMENTS

RESULT 1
LOCUS AF011757
DEFINITION Homo sapiens RAGE binding protein (P12) mRNA, complete cds.
ACCESSION AF011757
VERSION AF011757.1
KEYWORDS GI:2293532

Source	Organism	Human
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Li, J.F., ... Hofmann, M.A., Drury, S., Qu, X. and Schmidt, A.M.	
TITLE	Functional identification of a novel ligand for RAGE	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 405)	
AUTHORS	Li, J.F., ... Hofmann, M.A., Drury, S., Qu, X. and Schmidt, A.M.	
TITLE	Direct Submission	
JOURNAL	Submitted (30-JUN-1997) Physiology, Columbia University, 630 W. 168th St., New York, NY 10032, USA	
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gene	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
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CDS	/gene="P12"	
	1..279	
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	/protein_id="BAB65423.1"	
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	/translation="WTKLEHLEGIINIFHOYSVRVGHFDLNLKRELQITKELPKT LQNRKDOPTIDKIFQDDLDADKDGAVSFEEFVILVSRVLTAKHIDHKE"	
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Query Match	80.8%; Score 319.2; DB 10; Length 405;	
Best Local Similarity	95.1%; Pred. No. 1.2e-80;	
Matches 386; Conservative	0; Mismatches 8; Indels 12; Gaps 5;	
OY	1 atgactaagcttgagagacacacttgagaggaatcatcaaatcttcaccagatctccgtt 60	
DB	1 atgactaagcttgagagacacacttgagaggaatcatcaaatcttcaccagatctccgtt 60	
OY	61 cgggtgagagcatttcgacacacccctcaacaagcgctgagctgaagcagctgatacaaaagga 120	
DB	61 cgggtgagagcatttcgacacacccctcaacaagcgctgagctgaagcagctgatacaaa- gga 119	
OY	121 acttcccaaaacccctccagaaacccaagaacccaacctaccattgacaaataatcccaaga 180	
DB	120 acttcccaaaacccctccagaaacccaagaacccaacctaccattgacaaataatcccaaga 179	
DB	181 cctgtagtcggttaagaacgagcggtcagcttcgtgaagatccgtatcctgctgcag 240	
DB	180 cctgtagtcggttaagaacgagcggtcagcttcgtgaagatccgtatcctgctgcag 239	
OY	241 ggtgctgaagaaagccacatagatcatccacaagaagtatg-----ttccagcaagt 294	
DB	240 ggtgctgaagaaagccacatagatcatccacaagaagtatgaaagctctttccagcaagt 299	
OY	295 tcccaagaagactaacctctcctcctccctgagctg---ctcccgagaggaagaagaatt 351	
DB	300 ccccaagaagactaacctctcctcctccctgagctg---ctcccgagaggaagaagaatt 359	
OY	352 -ataaagctactctggcaaa-ttcttagcaaaaaaataaaaaa 395	
DB	360 aataaagctactctggcaaaagtcttagcaaaaaaataaaaaa 405	
RESULT	2	
LOCUS	D49548 429 bp mRNA MAN 10-FEB-1999	
DEFINITION	Bos taurus mRNA for calcium-binding protein in amniotic fluid 1, complete cds.	
ACCESSION	D49548	
VERSION	D49548.1 GI:1694616	
KEYWORDS	CAAF1, calcium-binding protein in amniotic fluid 1.	

Source	Organism	Reference Title	Authors	Journal	Medline	Features
Bos taurus	Bos taurus	Esophagus cDNA				
Bos taurus	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.	1 (bases 1 to 429)				
Hitomi, J.		Direct Submission				
Submitted (09-MAR-1995)		to the DDBJ/EMBL/GenBank databases. Jiro Hitomi, National Cancer Center Research Institute, Growth Factor Division, 5-1-1 Tsukiji, Chuo-ku, Tokyo 104, Japan (tel:03-3542-2511, Fax:03-3542-8170)				
2 (bases 1 to 429)						
Hitomi, J.		Unpublished (1996)				
3 (sites)						
Hitomi, J., Yamaguchi, K., Kikuchi, Y., Kimura, T., Maruyama, K. and Nagasaki, K.						
A novel calcium-binding protein in amniotic fluid, CAAF1: its molecular cloning and tissue distribution						
J. Cell. Sci. 109 (Pt 4), 805-815 (1996)						
69298783						
Location/Qualifiers						
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/db_xref="taxon:9913"						
/clone_id="fetal bovine esophagus cDNA"						
/dev_stage="fetus"						
/tissue_type="esophagus"						
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/gene="CAAF1"						
48..326						
/gene="CAAF1"						
/codon_start=1						
/product="calcium-binding protein in amniotic fluid 1"						
/protein_id="BA08496.1"						
/db_xref="GI:1694617"						
/translation="MTKLEDDHEGIIIFHOYSVNGHFDTLNKRELKDLTKELPPT LQNKDQPTIDKTFQDADKDGVSFEFEVIVSRVLTAKHIDHKE"						
BASE COUNT	130 a	111 c	97 g	91 t		
ORIGIN						
Query Match	77.0%	Score 304;	DB 3;	Length 429;		
Best Local Similarity	94.5%	Pred. 2.6e-76;				
Matches 361;	Conservative 0;	Mismatches 10;	Indels 11;	Gaps 4;		
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DB 48 atgactaagcttgggaagatcactctggagggaatcattcaacattcttcacacagttctcgtt						
QY 61 cgggttgggcatcttcgaacacctcaacaaggttagctgaagcaagctgatcacaaaggga						
DB 108 cgggttgggcatcttcgaacacctcaacaaggttagctgaagcaagctgatcacaaaggga						
QY 121 acttcccaaaaccttcgaagaccaccaagaaccaactcaactgacaaatatcccaaga						
DB 167 acttcccaaaaccttcgaagaccaccaagaaccaactcaactgacaaatatcccaaga						
QY 181 ccttgatgacgaataagacggagccgttcagcttgaaggaattcgttagtcctgtgtccag						
DB 227 ccttgatgacgaataagacggagccgttcagcttgaaggaattcgttagtcctgtgtccag						
QY 241 ggttgctgaagacccacatagatatcccaaaagagagg-----tttccacaatg						
DB 287 ggttgctgaagacccacatagatatcccaaaagagagagg-----tttccacaatg						
QY 295 tcccaagaagactacccttccttccttcaggtgc--tccccaagaagagagaatt						
DB 347 tcccaagaagactacccttccttccttcaggtgc--tccccaagaagagagaatt						
QY 352 -ataacgtactcttggcaaat 372						

DB 407 AATAACGTAAGTGGCAAGT 428

RESULT 3
ID E12013 standard; RNA; MAN; 429 BP.
XX E12013;
XX E12013.1
XX 07-OCT-1997 (Rel. 52, Created)
XX 08-OCT-1997 (Rel. 52, Last updated, Version 1)
DE cDNA encoding bovine CAAP1 (Calcium binding protein in Amniotic Fluid
DE 1).
XX JP 1996238090-A/2.
XX Bos taurus
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;
XX Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
XX [1]
XX 1-429
XX Hitomi J., Yamaguchi K., Yamamura T.;
XX "NEW CALCIUM-BINDING PROTEIN";
XX Patent number JP 1996238090-A/2, 17-SEP-1996.
XX HITOMI JIRO, TONEN CORP.
XX OS Bos taurus (bovine)
XX PN JP 1996238090-A/2
XX PD 17-SEP-1996
XX PF 06-MAR-1995 JP 1995045564
XX PI HITOMI JIRO, YAMAGUCHI KEN, YAMAMURA TOKUSHICU
XX PC C12N15/09, C07H21/04, C07K14/47, C07K19/00, C12N1/15, C12N1/19,
XX C12N1/21,
XX PC C12N15/10, C12P21/02, C12P21/08, G01N33/53, G01N33/574,
XX G01N33/577//A61K39/395,
XX PC A61K39/395, (C12N1/15, C12R1:69), (C12N1/19, C12R1:865), (C12N1/21,
XX C12R1:19),
XX PC (C12P21/02, C12R1:19), (C12P21/08, C12R1:91);
XX CC strandedness: Double;
XX CC topology: Linear;
XX CC hypothetical: No;
XX CC anti-sense: No;
XX FH Key
XX FH Location/Qualifiers
XX FT 1. 429
XX FT /organism="Bos taurus"
XX FT /cell-type="Amniotic fluid"
XX FT 5'UTR
XX CDS
XX FT 48..326
XX FT /product="Bovine CAAP1 (Calcium binding protein
XX in Amniotic
XX Fluid 1)"
XX FT 327..429
XX FH 3'UTR
XX FH Location/Qualifiers
XX FH 1. 429
XX FH /db_xref="taxon:9913"
XX FT /organism="Bos taurus"
XX XX
XX Sequence 429 BP; 130 A; 111 C; 97 G; 91 T; 0 other;

Query Match 77.0%; Score 304; DB 24; Length 429;
Best Local Similarity 94.5%; Pred. No. 2, 6e-76;
Matches 361; Conservative 0; Mismatches 10; Indels 11; Gaps 4;
QY 1 atgactaagctgagagccacctgaggaatcatcaacatctccacagctacgtt 60
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DB 407 AATAACGTAAGTGGCAAGT 428

RESULT 4
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XX E12020;
XX AC E12020;
XX XX
XX E12020.1
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XX 08-OCT-1997 (Rel. 52, Last updated, Version 1)
DE cDNA encoding bovine CAAP1 (Calcium binding protein in Amniotic Fluid
DE 1).
XX JP 1996238091-A/1.
XX OS Bos taurus
XX PN JP 1996238091-A/1
XX PD 17-SEP-1996
XX PF 06-MAR-1995 JP 1995070468
XX PI HITOMI JIRO, YAMAGUCHI KEN, KIMURA TATSUJI
XX PC C12N15/09, C07H21/04, C07K14/47, C07K16/18,
XX C12N1/21,
XX PC C12P21/02, C12P21/08, G01N33/53, G01N33/577//A61K39/395,
XX A61K39/395,
XX PC C12N5/10, (C12N1/21, C12R1:19), (C12P21/02, C12R1:91), (C12P21/02,
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XX CC topology: Linear;
XX CC hypothetical: No;
XX CC anti-sense: No;
XX FH Key
XX FH Location/Qualifiers
XX FT 1. 429
XX FT source

DB 48 ATGACTAAGCTGGAAGATCACTGGAGGAAATCATCAACTTCCACAGTACTCCGT 107

QY 61 cgagtgaggcattcgcagaccctcacaagaagcgtagctgaagcagctgatacaaga 120
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DB 108 CGGGTGGGGCATTTTCGACACCCCTTACACAGCGTAGCTGAGAGCTGATCACAAA 166
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QY 121 acttcccaaaacccctcagagacacccaagaacacacacacatcagacaatatccaga 180
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DB 167 ACTTCCAAAACCTCCAGAAACACCAAGATCAACCTACCATTCACAAAATATCCAGA 226
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QY 181 cctgatagccgataaagaagagccgctcagcttgcgaagtgcgtgctgctgctcag 240
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DB 227 CTTGGATGCCGATTAACACGAGCGCTCAGCTTGAAGAAATTCGTAGTCTGTGTCCAG 286
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QY 241 ggtgctgaaaaaacccacatagatccacaagaagtagt-----ttccagcaatgt 294
|||||
DB 287 GGTCTGAAAACAGCCACATAGATATCCACAAAGATAGGAAGCTTTTCCAGCAATGT 346
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QY 295 tcccaagaagactacccctcctccctgagctgc---tcccgaggagagaagaatt 351
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CC	FT	/cell_type="Amniotic fluid"
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CC	FT	48..326
CC	FT	/product="Bovine CAAF1(Calcium binding protein
CC	FT	in Amniotic
CC	FT	Fluid 1)"
CC	FT	327..429
XX	Key	Location/Qualifiers
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FT		/db_xref="taxon:9913"
FT		/organism="Bos taurus"
XX		
SQ	Sequence	429 BP; 130 A; 111 C; 97 G; 91 T; 0 other;
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Query Match		
Best Local Similarity 77.0%; Score 304; DB 24; Length 429;		
Matches 361; Conservative 94.5%; Pred No. 2.6e-76;		
Mismatches 0; Mismatches 10; Indels 11; Gaps 4		
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OY	61 cgggtggggcatlttcagacccctcaacaacgctgtagctgaagcagtgcatacaagaaga	120
DB	108 CGGTGGGGCATTTGCACACCTTCACAAGCGTAGCTGAAGCACCTGATCACAAA-GGA	166
OY	121 atttcccanaaaccttcacagaaacccaagaaccaactcacattgaaaaatatccaga	180
DB	167 ACTTCCCANAACCCTCCACAACACCAAGAATCACTACCATTAAGAAAAATATTCCAAG	226
OY	181 ccttgatgccgatataaagaaggagccgtcagcttggagaatcgttagtcctgctgcag	240
DB	227 CCTGATGCCGATAAAGAGGAGCCCTCAGCTTTGAGGAATTGTAAGTCTGCTGCTGCAG	286
OY	241 ggtgctgaaaaagccccacatatatccacaagaagtag-----ttccagaacagt	294
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OY	295 tcccaagaagaacttaccccttccttcctccctcgaagctgc---tcccgagggagagaatt	351
DB	347 CCCCAAGAAAGACTTACCCCTTCCTCCCTGAGAGCTCCTTACCAGGAGGAAGAGAATT	406
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XX	EI2012.1	
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XX	07-OCT-1997 (Rel. 52, Created)	
DT	08-OCT-1997 (Rel. 52, Last updated, Version 1)	
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DE	1).	
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XX	JP 1996238090-A/1.	
KW		
XX	Homo sapiens (human)	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;	
OC	Primates; Catarrhini; Homidae; Homo.	
XX	[1]	
RN	1-441	

RA	HITOMI J Yamaguchi K., Yamanura T.:
RT	"NEW CALCIUM-BINDING PROTEIN."
RL	Patent number JP 1996238090-A/1, 17-SEP-1996.
XL	HITOMI JIRO, IONEN CORP.
XX	
OS	Homo sapiens (human)
CC	PN JP 1996238090-A/1
CC	PD 17-SEP-1996
CC	PF 06-MAR-1995 JP 1995045564
CC	PI HITOMI JIRO, YAMAGUCHI KEN, YAMANURA TOKUSHIROU
CC	PC C12N15/09,C07H21/04,C07K14/47,C07K19/00,C12N1/15,C12N1/19,
CC	C12N1/21,
CC	PC C12N5/10,C12P21/02,C12P21/08,G01N33/53,G01N33/574,
CC	G01N33/577//A6IK39/395,(C12N1/15,C12R1:69),(C12N1/19,C12R1:865),(C12N1/21,
CC	A6IK39/395,(C12N1/15,C12R1:69),(C12N1/19,C12R1:865),(C12N1/21,
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CC	(C12P21/02,C12R1:19),(C12P21/08,C12R1:91);
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CC	/product="Human CNAFL(Calcium binding protein
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CC	Fluid 1)"
CC	FT Fluid 1) 301..441
CC	FT 3'UTR
XX	
XX	Key Location/Qualifiers
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FT	/organism="Homo sapiens"
XX	
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	Query Match 41.6%, Score 164.4; DB 24; Length 441;
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	Matches 215; Conservative 0; Mismatches 66; Indels 1; Gaps 1
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DB	22 ATGACAAAACCTTGAAGACCATCTGAGGGAAATTGCATATCTTCACCACAATCACTCAGTT 81
OY	61 cggagtggggcatctgcgaacccctcaacaagcgctgagctgaagcagctgatactcaagaagga 120
DB	82 CGGAAGGGGCGATTGTGACACACCTCTCTTAAGSGTGAGCTGAAGCACAGCTGCTTACAA- 140
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DB	141 GCTTCACAAACACCATCAGAATAATCAAAGATPAAGCTGTCATTGATGAATATTCCAAG 200
OY	181 cctgatatccgataagaagcaggaagccgctgaagcttcgaggaattcgtatgcttggtgtccag 240
DB	201 CCTGATATCTAATCAAGATGAACAGGTGACTTTCAAGATTCATATCCTCTGTAACCAT 260
OY	241 gttgctgaagaacgccacatagatatcacaaagaataggt 282
DB	261 TGCGCTGAAGGCTGCCATTACCAACACCACAAAGATAGGT 302
RESULT	6
D49549	D49549 442 bp mRNA PRI 10-FEB-1999
LOCUS	DEFINITION Homo sapiens mRNA for calcium-binding protein in amniotic fluid 1,
	complete cds.

AUTHORS	Yamamura, T.
TITLE	Direct Submission
JOURNAL	Submitted (22-FEB-1996) to the DDBJ/EMBL/GenBank databases. Tokujito Yamamura, National Cancer Center Research Institute, Growth Factor Division; 5-1-1 Tsukiji, Chuo-ku, Tokyo 104, Japan (E-mail: tyamamura@gen2.ncc.go.jp, Fax:4302)
REFERENCE	2 (bases 1 to 466)
AUTHORS	Yamamura, T.
JOURNAL	Unpublished (1996)
REFERENCE	3 (sites)
AUTHORS	Yamamura, T., Hitomi, J., Nagasaki, K., Suzuki, M., Takahashi, E., Saito, S., Tsukada, T. and Yamaeuchi, K.
TITLE	Human CAFL gene--molecular cloning, gene structure, and chromosome mapping
JOURNAL	Biochem. Biophys. Res. Commun. 221 (2), 356-360 (1996)
MEDLINE	96192053
FEATURES	Location/Qualifiers
source	1..466
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	69..347
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Query Match	41.6%; Score 164.4; DB 9; Length 466;
Best Local Similarity	76.2%; Pred. No. 1.5e-36;
Matches 215; Conservative	0; Mismatches 66; Indels 1; Gaps 1;
OY	1 atgactaaagctggaagacacacctggaagggaatcatcaaatcttccacagactcgtt 60
Db	69 atgacaaacttggaagagatctggaagggaattgtcaaatattctccaccaatatctcagt 128
OY	61 cgggtgaggcatcttcgacacccctcaacaagcgtgagctgaagcagctatcacaaagg 120
Db	129 cggaaaggcgattttgacacacctctctaaaggtgagctgaacacagctgttccaaa 187
OY	121 acttccaaaacccctcagaaacccaagaacccaacctaccattgacaaaatactcca 180
Db	188 gcttccaaaacccatcagaatgataatcaaaagatgaaactgtgattgaaatattccaa 247
OY	181 cctgataatcgataaagacggagccgctcagctcttgaagaaatcgtcagtcctggtc 240
Db	248 cctgataatcgataaagacggagacagctgacattgaaagattcatatccctggatgc 307
OY	241 ggtgctgaataacagcccatagatcatcacaaagatgagt 282
Db	308 tggcctgaaggctgcccatattaccacacccacaaagatgagt 349
RESULT	9
AF091848	355 bp mRNA
LOCUS	AF091848
DEFINITION	Oryctolagus cuniculus calgranulin C mRNA, partial cds.
ACCESSION	AF091848
VERSION	AF091848.1 GI:3661596
KEYWORDS	Oryctolagus cuniculus.
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
ORGANISM	Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE		1 (bases 1 to 355)	
AUTHORS		Yang,Z., deVeier,M.J., Gardiner,E.E., Devenish,R.J., Handley,C.J., Underwood,J.R. and Robinson,H.C.	
TITLE		Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfio-polymorphanin C when incubated with inorganic [35S] sulfate J. Biol. Chem. 271 (33), 19802-19809 (1996)	
JOURNAL MEDLINE		96355278	
REFERENCE		2 (bases 1 to 355)	
AUTHORS		Yang,Z., deVeier,M.J., Gardiner,E.E., Devenish,R.J., Handley,C.J., Underwood,J.R. and Robinson,H.C.	
TITLE		Submitted (15-SEP-1998) Biochemistry & Molecular Biology, Monash University, Wellington Road, Melbourne, Vic 3168, Australia	
FEATURES		Location/Qualifiers	
SOURCE		1..355	
CDS		/organism="Oryctolagus cuniculus"	
		/strain="New Zealand white"	
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Query Match		32.7%, Score 129.2; DB 3; Length 355;	
Best Local Similarity		64.0%; Pred. No. 1.5e-26;	
Matches 228; Conservative		0; Mismatches 123; Indels 5; Gaps 2;	
OY	34	atcaacatcttcaccagttactcgttggggtggcgatttgacacctcaagaagt 93	
Dd	1	ATCAATATCTTCACAGTACAGTCACTGCGCACGGGGCATATGACACCTGTCCAAGTGC 60	
OY	94	gaagctgaagcaagctgatcacaaagaagtaattccaaaacctccagaacaccaaagacca 153	
		'	
Dd	61	GAGCTGAAGAAGACTATCAG-CACGGAACCTGCTGAACACATCAAGAACACCAAAGATCA 119	
OY	154	acctaacattgcacaataattccaagaacctgtgattcgcataaagaaggagccgttagctt 213	
		'	
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Dd	180	CAGAAGATTCCTCGTCCCTGCTGGCTCTGTGTGTGTGACTGCTCATGAGAAATCATCACAA 239	
OY	274	aagaagagtttcacgaatgt-----tcccaagaagaacttacacctctctcccttagagct 329	
Dd	240	AGAGTAGCAAGCGCTCTAGTGATATGCCCAAGGGCCCTTACTCTCCATCAAAAGCCAG 299	
OY	330	gtcccccgaggagagagaatataaacytactttggcaaatlcttagcaaaaaaa 385	
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Dd	300	CCTTCCCGAGGAGTAGTGTAATAAAGTACTCATGAAGAGCTTAATAAAAAAAA 355	
RESULT 10			
LOCUS	GGI26MRP	598 bp mRNA VRT	28-APR-1992
DEFINITION	G.gallus 126 MRP mRNA.		
VERSION	X61200		
KEYWORDS	X61200.1 GI:62998		
ORGANISM	chicken. Gallus gallus Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. Graf,T.H.		
REFERENCE		1 (bases 1 to 598)	

TITLE	Direct Submission
JOURNAL	Submitted (01-AUG-1991) T.H. Graf, EMBL, Meyerhofstr. 1, 6900 Heidelberg, FRG
REFERENCE	2 (bases 1 to 598)
AUTHORS	Nakano,T. and Graf,T.
TITLE	Identification of genes differentially expressed in two types of v-myb-transformed avian myelomonocytic cells
JOURNAL	Oncogene 7 (3), 527-534 (1992)
MEDLINE	92195690
FEATURES	Location/Qualifiers
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BASE COUNT	158 a 198 c 129 g 113 t
ORIGIN	

Query Match	22.1%	Score 87.2	DB 4	Length 598
Best Local Similarity	60.6%	Pred. No	1.4e-14	
Matches 160; Conservative	0	Mismatches 103	Indels 1	Gaps 1

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Db	79	AGCTGGAGAAAAGCCATTGATGTCATCATTCGATGCTTCCACCAAGTACTGAGACGGGAGG	138
QY	68	ggcatttcgacacccctcaacaaagcgttgagctgtaagcagctgtgatacaaaagggaactccg	127
Db	139	GGGACAAAGACACCCCTGTAGCCAGGAGAGAGACTAAGCTTTGAT-TGAGAGCAGCTTGCC	197
QY	128	aaaacccttcagaaacacccaagaaccaactaccatctgtacaaaatatctcaagacctgagt	187
Db	198	AACATCCGTGAACACAGTGAAGATAGCTCTTATTCGACCAATCTTCAAGATCTCGAT	257
QY	188	gocsgataaagagagagcgctcagctcttgaggaatcgtgatctcgtgtgcgaaggtgtcgtg	247
Db	258	AACACAAAGAGACCAAGCAGCTGAGCTTTGGTGAAGTATCTCTGTATCATCCGGGGTAC	317
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Db	318	GTGCGCACCCACGAGCACCCTCCAC	341

RESULT 11			
HSS1002			
LOCUS	HSS1002	532 bp	DNA
DEFINITION	H.sapiens S100A12 gene, exon 2.		
			PRI
			11-AUG-1997

SESSION X98289
SESSION X98289.1 GI:1545949
KEYWORDS X98289.1
SOURCE calcium-binding protein; Calgranulin C; S100A1; gene.
human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 532)
Wicki, R.
Direct Submission
Submitted (04-JUN-1996) R. Wicki, Department of Pediatrics,

REFERENCE	AUTHORS	TITLE
2 (bases 1 to 532)	Wicki, R., Marenholz, I., Mischke, D., Schaefer, B. W., and Heilmann, C. W.	Characterization of the human S100A12 (calgranulin C, p6, CAFL1, CGRP) gene, a new member of the S100 gene cluster on chromosome 1q21

JOURNAL	Cell Calcium 20 (6), 459-464 (1996)
MEDLINE	97138564
COMMENT	Overlaps with X97859.
FEATURES	Location/Qualifiers
source	1..532

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/db_xref="taxon:9606"

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    /tissue_type="breast"
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BASE COUNT      154 a      129 t
ORIGIN

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Query Match	21.88;	Score 86;	DB 9;	Length 532;
Best Local Similarity	83.18;	Pred. No. 3.1e-14;		
Matches 98;	Conservative 0;	Mismatches 20;	Indels 0;	Gaps 0;

[illegible]

RESULT	12
D83657	
LOCUS	
DEFINITION	D83657 4092 bp DNA PRI 06-FEB-1999
	Human DNA for CAAFI (calcium-binding protein in amniotic fluid 1), complete cds.

ACCESSION	D83657
VERSION	D83657.1
KEYWORDS	GI.1502284 CAAF1 (calcium-binding protein in amniotic fluid 1); S100 protein family.
SOURCE	Homo sapiens adult DNA.
ORGANISM	Homo sapiens

REFERENCE
TITLE
AUTHORS
JOURNAL

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 4092)
Yamamura,T.
Direct Submission
Submitted (22-FEB-1996) to the DDBJ/EMBL/Genbank databases.
Tokutiro Yamamura. National Cancer Center Research Institute

REFERENCE
AUTHORS
JOURNAL
REFERENCE

Growth Factor Division, 5-1-1 Tsukiji 1, Chuo-ku, Tokyo 104, Japan
(E-mail: tyamamura@gan2.ncc.go.jp, Fax:4302)
2 (bases 1 to 4092)
Yamamura, T.
Unpublished (1996)
3 (sites)

AUTHORS	Yamamura, T., Hitomi, J., Yamaguchi, K., Suzuki, M., Takahashi, E., Saito, S., Tsukada, R., and Yamaguchi, K.
TITLE	Human CAMEL gene-molecular cloning, gene structure, and chromosome mapping
JOURNAL MEDLINE	Biochem. Biophys. Res. Commun. 221 (2), 356-360 (1996)
FEATURES	96192053 Location/Qualifiers

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1971. .1976
TATA_signal
exon
2001. .2048
/number=1

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GenCore version 4.5
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OK nucleic - nucleic search, using sw model

Run on: March 14, 2000, 15:47:30 ; Search time 56.66 seconds
(without alignments)
1744.191 Million cell updates/sec

Title: US-09-167-705-1

Perfect score: 395
Sequence: 1 atgactaagctggaggacca.....agcaaaaaaaaaaaaaaa 395

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Number of hits satisfying chosen parameters: 623170

Total number of hits satisfying chosen parameters: (623170)

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	304	77.0	429	1 T39345	Calcium binding pr
2	166	42.0	273	1 T62569	DNA encoding compo
3	164.4	41.6	440	1 T39346	Calcium binding pr
4	164.4	41.6	479	1 T85774	Human chemotactic
5	75.6	19.1	571	1 V34698	Human calprotectin
6	63.8	16.2	150	1 V87807	EST clone EH78. Ne
7	61.4	15.5	408	1 V34697	Human calprotectin
8	59	14.9	303	1 Q20506	Human mts-1 coding
9	59	14.9	303	1 Q99177	Human mts-1 gene.
10	58.8	14.9	4440	1 T68322	Human multidrug re
11	54.2	13.7	579	1 Q99178	Human mts-1 CDNA.
12	53.4	13.5	488	1 T20500	Human gene signatu
13	51.6	13.1	433	1 Q23343	Murine CP-10. New
14	49.8	12.6	4195	1 T68321	Human multidrug re
15	41.8	10.6	10952	1 T33345	Human CAPL gene. S
16	41.8	10.6	10952	1 V41162	Human CAPL gene.
17	41.8	10.6	10952	1 X17696	Human CAPL genomic
18	41.6	10.5	254	1 T20087	Human gene signatu
19	39.6	10.0	350	1 X23464	Human neutrophil c
20	35.2	8.9	452	1 Q28007	Sequence encoding
21	35.2	8.9	452	1 Q28760	Sequence of clone
22	35.2	8.9	600	1 V86185	EST clone J635. Ne
23	34	8.6	1080	1 V73498	Human S100P1 DNA.
24	33.8	8.3	447	1 Q04331	Recombinant calmod
25	32.8	8.3	504	1 Q04332	Plasmid pOCAL7 con
26	32.8	8.3	654	1 Q04332	Plasmid pRCM1 and
27	32.4	8.2	4160	1 V41884	Nucleotide sequence
28	31.8	8.1	861	1 Q99552	Thrombospondin cod
29	31.4	7.9	3175	1 V34323	Human secreted pro
30	31.4	7.9	3259	1 V34306	Human secreted pro
31	31.2	7.9	243	1 Q57430	Ca binding protein
32	31.2	7.9	532	1 T85298	Human chemotactic
33	31.2	7.9	673	1 X39799	Gastric cancer ass
34	31.2	7.9	1141	1 V73499	Human S100P2 DNA.

35	31.2	7.9	1543	1 X27326	Human secreted pro
36	31.2	7.9	110000	1 V30458.1	Continuation (2 of
37	31.2	7.9	110000	1 V30459.1	Continuation (2 of
38	31	7.8	2349	1 V80608	Kidney injury asso
39	31	7.8	4590	1 N60472	Sequence encoding
40	30.8	7.8	573	1 X39800	Gastric cancer ass
41	30.6	7.7	173	1 V00432	3' fragment of clo
42	30.6	7.7	173	1 T91309	Human H83-22 secre
43	30.6	7.7	463	1 Q68827	hg14 clone showing
44	30.6	7.7	1078	1 T91308	Human H83-22 secre
45	30.6	7.7	5194	1 X25885	C.albicans alpha-I

ALIGNMENTS

RESULT 1	
T39345	T39345 standard; CDNA; 429 BP.
AC	T39345;
DT	01-MAY-1997 (first entry)
DE	Calcium binding protein CAPL coding sequence.
KW	Calcium binding protein; bovine; amniotic fluid; S100 protein family;
KW	Intracellular signal transduction; squamous epithelial cell; neutrophil;
KW	macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;
KW	squamous cell carcinoma; skin; oesophagus; CAPL; lung; blood disease;
OS	Bos taurus.
FH	Key
FT	Location/Qualifiers
FT	cds 48..326
FT	/tag= a
FT	/product= calcium binding protein

PD	EP-731166-A2.
PD	11-SEP-1996.
PF	04-DEC-1995; 119045.
PR	06-MAR-1995; JP-070468.
PR	06-MAR-1995; JP-045564.
PA	(HIRO) HIROMI J.
PA	(TOFU) TONEN CORP.
PI	Hitomi J, Kimura T, Yamaguchi K, Yamamura T;
PI	WPI; 96-403989/41.
DR	P-PDB; W03563.
DK	New human or bovine calcium binding protein and related nucleic acid
PT	- is a marker for inflammation, neoplasia, skin and blood diseases
PS	Claim 1: Page 21; 36pp; English.
CC	This sequence represents the coding sequence for the CAPL
CC	calcium-binding protein isolated from bovine amniotic fluid. CAPL
CC	belongs to the S100 protein family, which includes calyculin, MRP8, and
CC	MRP14. Intracellular calcium ion concentration is one of the key factors
CC	for intracellular signal transduction. The calcium signals are
CC	transduced by various calcium-binding proteins, such as the protein
CC	encoded by this sequence. CAPL is normally expressed in squamous
CC	epithelial cells, neutrophils and macrophages, but atypical epithelial
CC	cells are negative for CAPL and overexpression is observed in several
CC	types of cancer cells and neutrophils/macrophages infiltrating cancerous
CC	lesions. Detection of CAPL (using antibodies in usual immunoassays) can
CC	be used to diagnose (or monitor) inflammation, neoplasia (particularly
CC	squamous cell carcinoma of the skin, oesophagus, lung and cervix), and
CC	skin and blood diseases.
SQ	Sequence 429 BP; 130 A; 111 C; 97 G; 91 T;

Query Match 77.0%; Score 304; DB 1; Length 429;
Best Local Similarity 94.5%; Fred. No. 7.6e-81;
Matches 361; Conservative 0; Mismatches 10; Indels 11; Gaps 4;

QY	1 atgactaagctggaggaccactggaggaatcatcacaatcttcacacagatccgtt 60
DB	
DB	48 atgactaagctggaggaccactggaggaatcatcacaatcttcacacagatccgtt 107
QY	61 cgggtgggacatttcgacacccctcaacaagcgtgagctgaagcagctatcacaaagga 120
DB	
DB	108 cgggtgggacatttcgacacccctcaacaagcgtgagctgaagcagctatcacaaagga 166

Qy	121	acttcccaaaacccctccgcagacaccaaagacaaaccctacacattgacaaaatattccaga	180
Db	167	acttcccaaaacccctccgcagacaccaaagacaaaccctacacattgacaaaatattccaga	226
Qy	181	ccctgatagcgataaagaacggaacgcgtcaagctttgaaagaaatcgttagtctcgtgltccag	240
Db	227	cctggatgtcccatataagacgagccgcgtcagctttgaaagaaatcgttagtctcgtgltccag	286
Qy	241	ggtctgtaaaacagcccaatagatattccaaagaagttag-----ttccagaacatgt	294
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Qy	295	tcccaagaagaacttacccttccttcctctgaagctgc--tcccgaagggaagagaat	351
Db	347	ccccaaagaaagacttacccttctcctcctgagctgccttaccgaggaaggaagagaaat	406
Qy	352	-ataaagctactcttggcaaat	372
Db	407	ataaagctactcttggcaaat	428

ID	PT	2	1
T62569			
AC	T62569	standard; DNA; 273 BP.	
DE	16-OCT-1997	(first entry)	
DE	DNA encoding component of bioactive metal RNA polypeptide.		
KW	Bioactive; metal; RNA polypeptide; RNP; modulation; analysis;		
KW	angiogenesis; vascular state; mammalian tissue; transfer; cell;		
KW	leukocyte; pig; monocytic-CuRNP; ss.		
OS	Sus scrofa.		
FT	Key	Location/Qualifiers	
FT	mat_peptide	1..272	
PN	DE19628895-A1.	/*tag= a	
PD	23-JAN-1997.		
PF	17-JUL-1996; 028895.		
PR	18-AUG-1995; DE-030500.		
PR	17-JUL-1995; DE-025992		
PA	(FRAU) FRAUHOFFER GES FORDERUNG ANGEWANDTEN.		
PI	Helmyer LMG, Kieseewetter S, Logemann E, Wisler JH;		
DR	Wpi: 97-088586/09.		
DR	P-PSDB: W01826.		
PT	Bioactive metal RNA polypeptide - useful for modulating		
PT	angiogenesis, etc.		
PS	Disclosure; page 2; 16pp; German.		
CC	A novel bioactive metal RNA polypeptide (RNP) has a RNA component		
CC	including the sequence T62568 and a polypeptide component having		
CC	the sequence W01826, which is encoded by T62569. The RNP, or		
CC	anti-RNP immunoglobulins, can be used to modulate and/or analyse		
CC	angiogenesis and the vascular state of mammalian tissue; transfer		
CC	genetic information in cells and selectively alter the nucleic		
CC	acid content of cells.		
CC	Leukocytes from pig's blood were cultured in medium, and the		
CC	supernatant treated with NH4 sulphate at 35, 45 and 90% saturation		
CC	to precipitate protein fractions. The residual supernatant was		
CC	diluted to 45% NH4 sulphate saturation and concentrated by		
CC	ultrafiltration using a 0.5 kD membrane. The retentate was purified		
CC	to give 8 mg of product described as monocytic-CuRNP.		
CC	Sequence 273 BP; 77 A; 78 C; 72 G; 46 T;		

Query Match	42.0%;	Score 166;	DB 1;	Length 273;
Best Local Similarity	77.7%;	Pred. NO. 4e-40;		
Matches 213; Conservative	0;	Mismatches 60;	Indels 1;	Gaps 1;

[illegible]

Accession	Sequence	Position
Db	61 CTGGGGCCACTATGACACCCCTGATCAACGGGAGGTGAAAGCAGCGTATCACCA - GGAAGCT	11.9
QY	124 tcccaaaacccctccagaacacccaagaaccaactaccattgacaaaatalctcaagact	183
Db	120 GCCCAACCCCTGAAAGAACCAAGACACGAGGACCATTTGACACAGATCTCCAGAAACCT	17.9
QY	184 gaaatgcgataaagaacggaagccgctcagactttgagaaatctgtagtcctggtgtccaggt	24.3
Db	180 GGATGCGCAACGAGATGAGCAGGTGTCTTTCAGAGATTTGTGTGTGTGACAGATGT	23.9
QY	244 gctgaaacagcccacatagatatccacaagaag	27.7
Db	240 GCTGATCACAGCCCATGACCAACATCCACAAAGAG - 273	

RESULT	3
ID	T39346
AC	T39346; standard; cDNA; 440 bp.
DT	01-MAY-1997 (first entry)
DE	Calcium binding protein CNAFL coding sequence.
KW	Calcium binding protein; human; amniotic fluid; S100 protein family;
KW	Intracellular signal transduction; squamous epithelial cell; neutrophil;
KW	macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;
KW	squamous cell carcinoma; skin; oesophagus; CNAFL; lung; blood disease;
OS	ds.
OS	Homo sapiens.
FT	Key
FT	Location/Qualifiers
FT	cds
FT	22..300
FT	/*tag= a
FT	/product= calcium binding protein
PN	EP-731166-A2.
PD	11-SEP-1996.
PE	04-DEC-1995; 119045.
PR	06-MAR-1995; JP-070468.
PR	06-MAR-1995; JP-045564.
PA	(H170) HITOMI J.
PA	(T070) TONEN CORP.
PI	Hitomi J, Kimura T, Yamaguchi K, Yamamura T;
DR	WPI: 96-403989/41.
DR	P-PSDB: W03564.
PT	New human or bovine calcium binding protein and related nucleic acid
PT	- is a marker for inflammation, neoplasia, skin and blood diseases
PS	Claim 1: Page 24; 36pp; English.
CC	This sequence represents the coding sequence for the CNAFL
CC	calcium-binding protein isolated from human amniotic fluid. CNAFL
CC	belongs to the S100 protein family, which includes calyculin, MRP8, and
CC	MRP14. Intracellular calcium ion concentration is one of the key factors
CC	for intracellular signal transduction. The calcium signals are
CC	transduced by various calcium-binding proteins, such as the protein
CC	encoded by this sequence. CNAFL is normally expressed in squamous
CC	epithelial cells, neutrophils and macrophages, but atypical epithelial
CC	cells are negative for CNAFL and overexpression is observed in several
CC	types of cancer cells and neutrophils/macrophages infiltrating cancerous
CC	lesions. Detection of CNAFL (using antibodies in usual immunoassays) can
CC	be used to diagnose (or monitor) inflammation, neoplasia (particularly
CC	squamous cell carcinoma of the skin, oesophagus, lung and cervix), and
CC	skin and blood diseases.
CC	Sequence 440 bp; 148 A; 98 C; 90 G; 104 T;

Query Match	41.6%;	Score 164.4;	DB 1;	Length 440;
Best Local Similarity	76.2%;	Pred. No. 1.4e-39;		
Matches 215; Conservative	0;	Mismatches 66;	Indels 1;	Gaps 1

[illegible]


```
OY 121 acttcccaaacctcccaaaccaaacacacacattgacaaatattccaaga 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 141 GGTGTAACACACATCAAGAAATATCAAGTATGATGAGAAATATCCAGG 200
OY 181 cctgtagtcgataaagaagcgcgtcagcttggaattcgtgtcgttcag 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 201 CCGTGAATGCTAATCAAGATGAAACAGTCTGACTTCAAGATTCATATCCTGTACCAT 260
OY 241 ggtgctgaataaagccacatagatatccaaagaagtagt 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 261 TGGCTGAAGGCTGCCATTACCAACCCACAAAGAGTAGT 302

RESULT 4
ID T85774 standard; DNA; 479 BP.
AC T85774; 28-JAN-1998
KW Human chemotactic cytokine I DNA.
KM chemotactic cytokine; tumour; autoimmune disease; antagonist;
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 76..354
     /tag= a
     /product= chemotactic_cytokine_I
PN MO9723640-A1.
PD 03-JUL-1997.
PF 26-DEC-1995; U16871.
PR 26-DEC-1995; WO-U16871.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Alfonso P, Gentz R, N1 J, Su JY, Yu G;
DR WPI: 97-351075/32.
P-PSDB: W24137.
PT DNA encoding chemotactic cytokine I - used to treat e.g. tumours,
PT chronic infection, leukaemia, etc.
PS Claim 4; Pages 48-49; 64pp; English.
CC This DNA sequence encodes the human chemotactic cytokine I polypeptide.
CC The DNA was amplified using PCR primers and restriction enzyme sites
CC were introduced by adding nucleotides corresponding to the chemotactic
CC cytokine I gene to the 5' and the 3' sequences. The DNA was cloned into
CC the bacterial expression vector pQE-9, along with a histidine tag and a
CC RBS. The resulting vector was used to transform the E. coli strain
CC M15/rep4. The transformants were identified and clones containing the
CC desired constructs were grown in liquid culture in LB media. The cells
CC were harvested by centrifugation and solubilised. The chemotactic
CC cytokine was purified from this solution by chromatography. This
CC polynucleotide, along with a vector and a host cell can be used for the
CC recombinant production of the chemotactic cytokine. Cytokine agonists
CC and antagonists can be used for the treatment of a patient requiring a
CC chemotactic cytokine I and for the treatment of a patient requiring a
CC inhibition of a chemotactic cytokine I polypeptide, respectively. The
CC chemotactic cytokine I is used to treat tumours, chronic infection,
CC leukaemia and T-cell mediated autoimmune diseases.
SQ Sequence 479 BP; 137 A; 113 C; 109 G; 120 T;

Query Match 41.6%; Score 164.4; DB 1; Length 479;
Best Local Similarity 76.2%; Pred. No. 1.5e-39;
Matches 215; Conservative 0; Mismatches 66; Indels 1; Gaps 1;
```

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OY 181 cctgtagtcgataaagaagcgcgtcagcttggaattcgtgtcgttcag 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 255 CCGTGAATGCTAATCAAGATGAAACAGTCTGACTTCAAGATTCATATCCTGTACCAT 314
OY 241 ggtgctgaataaagccacatagatatccaaagaagtagt 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 315 TGGCTGAAGGCTGCCATTACCAACCCACAAAGAGTAGT 356

RESULT 5
ID V34698 standard; CDNA; 571 BP.
AC V34698;
DT 03-SEP-1998 (first entry)
DE Human calprotectin subunit MRP-14 protein encoding CDNA.
KW Human; MRP-8; MRP-14; calprotectin; mineral precipitate; struvite;
KW calcium phosphate; kidney stone; renal calculi; struvite stone;
KW urinary tract infection; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 44..385
     /tag= a
     /product= "human MRP-14"
PN US5776348-A.
PD 07-JUL-1998.
PF 07-FEB-1995; 385241.
PR 07-FEB-1995; US-385241.
PA (MAST) MASSACHUSETTS INST TECHNOLOGY.
PI Asakura H, Dretler SP, Orme-Johnson WH, Selengut JD;
DR WPI: 98-397914/34.
P-PSDB: W60178.
PT Inhibiting kidney stone formation - uses the protein calprotectin
PT Example 1; Columns 23-24; 19pp; English.
CC This CDNA encodes a human calprotectin subunit MRP-14. This is used in
CC a method for inhibiting the formation of a mineral precipitate in a
CC solution which comprises providing a solution comprising component ions
CC of the mineral precipitate or its precursors and contacting the solution
CC with an effective amount of isolated calprotectin, or a derivative of it.
CC The method is useful for the inhibition of kidney stone formation (renal
CC calculi). Kidney stones are concentrations of inorganic and organic salts
CC that develop through crystal nucleation, aggregation and growth in the
CC kidneys, which then can block the ureter and if not passed to the
CC bladder, grow and become symptomatic. Struvite stones (MgNH4PO4) are
CC commonly found after urinary tract infection. The mechanisms of this and
CC other stone formation is unclear, but some urine compositions are known
CC to inhibit formation. One of the major components of these is a protein
CC factor calprotectin, which inhibits mineral precipitation. Calprotectin
CC can also be used to raise antibodies, which in turn can be used to detect
CC the protein in samples. The levels of calprotectin found in samples can
CC be compared to levels found in normal humans, and thus assuming increased
CC calprotectin correlates to indication of kidney stone formation, this
CC procedure can be used as a diagnostic tool.
SQ Sequence 571 BP; 160 A; 160 C; 157 G; 94 T;

Query Match 19.1%; Score 75.6; DB 1; Length 571;
Best Local Similarity 59.4%; Pred. No. 2.8e-13;
Matches 165; Conservative 0; Mismatches 109; Indels 4; Gaps 2;
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DB 235 GGAACCTGGACAAATGACAGACAGCTGAGCTTCGAGGATCATGCTGATGGC 294
QY 238 cagggtgcctgaacacagccacatagatatccacaag 275
DB 295 GAGGCTAACCTGGGCTCTCCACAGAGAGATGCACGAGG 332

RESULT 6
V87807/c
ID V87807 standard; cDNA: 150 BP.
AC V87807:
DE 12-FEB-1999 (first entry)
DE EST clone EH78.
KW Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolytics;
KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
OS Homo sapiens.
PN WO945437-A2.
PI 15-OCT-1998.
PI 10-APR-1998; U06956.
PI 10-APR-1997; US-837312.
PI (GENY) GENETICS INST INC.
PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Nerberg D,
PI Racie JA, Spaulding V, Treacy M;
PI WPI: 99-070078/06.
PI New polynucleotides encoding human secreted proteins - derived from
PI e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PI ovary, pituitary, retina and colon cDNA libraries
PI Claim 1; Page 186; 641pp: English.
CC The present sequence represents an expressed sequence tag (EST), and is
CC a polynucleotide of the invention. The polynucleotides of the invention
CC are all secreted EST sequences isolated from a variety of human tissue
CC sources. The EST sequences and proteins encoded by them are predicted to
CC have useful biological activities which would make them suitable for
CC treating, preventing or ameliorating medical conditions in humans and
CC animals, although no supporting data is given. Suggested activities
CC include nutritional activity, immune stimulating or suppressing activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity. The EST sequences are also stated to be useful for gene
CC therapy.
SQ Sequence 150 BP: 33 A; 36 C; 33 G; 48 T;
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KM urinary tract infection; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT 57..338
FT CDS /tag=a
FT /product="human MRP-8"
PN US5776348-A.
PI 07-JUL-1998.
PI 07-FEB-1995; 385241.
PI 07-FEB-1995; US-385241.
PI (MASI) MASSACHUSETTS INST TECHNOLOGY.
PI Asakura H, Drexler SP, Orme-Johnson WH, Selengut JD;
PI WPI: 98-397914/34.
PI P-PSDB: W60177.
PI Inhibiting kidney stone formation - uses the protein calprotectin
PI Example 1; Columns 21-22; 19pp: English.
CC This cDNA encodes a human calprotectin subunit MRP-8. This is used in
CC a method for inhibiting the formation of a mineral precipitate in a
CC solution which comprises providing a solution comprising component. Ions
CC of the mineral precipitate or its precursors and contacting the solution
CC with an effective amount of isolated calprotectin, or a derivative of it.
CC The method is useful for the inhibition of kidney stone formation (renal
CC calculi). Kidney stones are concentrations of inorganic and organic salts
CC that develop through crystal nucleation, aggregation and growth in the
CC kidneys, which then can block the ureter and if not passed to the
CC bladder, grow and become symptomatic. Struvite stones (MgNH4PO4) are
CC commonly found after urinary tract infection. The mechanisms of this and
CC other stone formation is unclear, but some urine compositions are known
CC to inhibit formation. One of the major components of these is a protein
CC factor calprotectin, which inhibits mineral precipitation. Calprotectin
CC can also be used to raise antibodies, which in turn can be used to detect
CC the protein in samples. The levels of calprotectin found in samples can
CC be compared to levels found in normal humans, and thus assuming increased
CC calprotectin correlates to indication of kidney stone formation, this
CC procedure can be used as a diagnostic tool.
SQ Sequence 408 BP: 118 A; 91 C; 106 G; 93 T;
```

Query Match 15.5%; Score 61.4; DB 1; Length 408;
Best Local Similarity 54.9%; Pred. No. 3.9e-09;
Matches 151; Conservative 0; Mismatches 111; Indels 13; Gaps 1;

```
QY 2 tgactaagctggagagacacactggaggaatcatcaactctccacagctactcgttc 61
DB 61 TGACCGAGCTGGAGAAACCTTGAACTCATCATGAGCTGACCAACAGTACCTCCGTA 120
QY 62 gggtagggcatttgacacccctcacaaagcgtgagctgaagcagctgtatccaaaggaa 121
DB 121 TAAAGGGGAATTCATGCGCTGTACAGGAGAGACTGAAGAAATTGCTAGAGACCGAGT 180
QY 122 ctcccaaaacccctcacaaagcacaacactacattgacaaataattccaagac 181
DB 181 GTCCTCAGATATTCAGGAAAGAGGTGCA-----GAGCTGTGTTCAAAAG 227
QY 182 ctgattgcgataaagacgagcgctcagctttgaggaattcgtagctcgtgtcagg 241
DB 228 TTGGATATCAACACATGAGTGTCAGTAACTTCCAGGAGTTCCTCATCTGTGATTAAG 287
QY 242 gtcgtgaacacgcccacatgatattccacaaga 276
DB 288 ATGGGCGTGGCAGCCCAAAAAAGCCATGAAGA 322
```

RESULT 8
Q20506
ID Q20506 standard; cDNA: 303 BP.
AC Q20506:
DE 14-MAY-1992 (first entry)
DE Human mts-1 coding region.
DE Metastatic cancer; antibodies; mouse; lung; liver; kidney; thyroid;
KW breast cancer; cell growth; 18A2; p8ka; ss.
OS Homo sapiens.
FH Key Location/Qualifiers

FT cds CDS 1.303
 FT /*tag= a
 FT /label= mts-1
 FT misc.binding 66.103
 FT /*tag= b
 FT /note= "encodes calcium binding domain"
 PN M09200757.A.
 PD 23-JAN-1992.
 PR 09-JUL-1991; U04832.
 PR 09-JUL-1990; US-550600.
 PA (RESE) RES CORP TECHN INC.
 PI Zain S. Lukandin E;
 DR WPI: 92-056647/07.
 DR P-PSDB: R20560.
 PT Metastatic cancer diagnosis by detection of mts-1 gene or protein
 PT - using antibody treatment of cancer and tumours of e.g. kidney,
 PT thyroid, lung and liver
 PS Claim 5; Fig 1; 82pp; English.
 CC A human cDNA library was constructed in lambda gt10 using poly A+
 CC RNA extracted from HeLa cells. The library was screened with mouse
 CC mts-1 cDNA probes (mouse mts-1 gene known as 18A2 has been
 CC previously isolated by Linzer et al., Proc. Natl. Acad. Sci. USA 80:
 CC 4271-4275, 1983) and strongly hybridising cDNA clones were
 CC sequenced, revealing a full length cDNA sequence (shown). Mts-1
 CC nucleic acid and antibodies derived from it are useful in the
 CC diagnosis of metastatic cancer, e.g. lung, kidney, thyroid or breast
 CC cancer. Cell lines capable of expressing mts-1 are useful as model
 CC systems for in vitro and in vivo anti-metastasis drug screening.
 CC Pharmaceutical comps. contg. the mts-1 protein or anti-cancer
 CC reagents mat be used to promote cell growth, or for treating cancer,
 CC respectively.
 SQ Sequence 303 BP; 83 A; 72 C; 87 G; 61 T;

Query Match 14.9%; Score 59; DB 1; Length 303;
 Best Local Similarity 56.3%; Pred. NO. 1.8e-08;
 Matches 130; Conservative 0; Mismatches 100; Indels 1; Gaps 1;

OY 10 ctggaggaaccacccatggaaggaatcatcaacatctccaccagtaactcgttcgggtggg 69
 DB 13 CTGGAGGAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAAGTACTCCGGCAAAGGGT 72
 OY 70 cattcgacacccctaaacagcgctgaagcagctgatacaaaaggaacttcccaa 129
 DB 73 GACAAGTTCAAGCTCAACAGATGATGAGCTAAAGAGCTGCTGACCC-35GAGCTGCCAG 131
 OY 130 aacctccgaacacccaagaccactacatctgacaaaatattccaagacctgagtc 189
 DB 132 CTTCCTGGGAAAGACAGATGATGAGCTCTTCCAGAAAGCTGATGACACTTGGACAG 191
 OY 130 cgataaagcggagccgctcagcttgaggaattcgtagtcctggttcag 240
 DB 192 CAACAGGACACAGAGGTGGACTTCCAGAGTACTGTGTCTTCCTCTG 242

RESULT 9
 ID 099177
 AC 099177:
 DI 27-DEC-1995 (first entry)
 DE Human mts-1 gene.
 KW Metastasis; cancer; mts-1 gene; tumour; therapy; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 1.303
 FT /*tag= a
 FT W09520656-A1.
 PD 03-AUG-1995.
 PR 31-JAN-1995; U01214.
 PR 31-JAN-1994; US-190560.
 PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
 PI Lukandin E, Zain S;
 DR WPI: 95-275441/36.

DR P-PSDB: R80453.
 PT Nucleic acid encoding human mts-1, antigenic fragments and
 PT antibodies - useful for diagnosis of malignant cancer and metastatic
 PT potential of tumour cells.
 PS Claim 15; Page 92; 124pp; English.
 CC A human cDNA library was constructed in lambda-gt10 using poly(A)+
 CC RNA prep'd. from HeLa cells. The library was screened with a 33p-
 CC labeled mouse mts-1 vDNA probe. A clone was obt'd. which comprised
 CC the full-length human mts-1 gene. The gene can be used to express
 CC mts-1 protein, e.g. in Sf21 cells, and antisense constructs are used
 CC to inhibit metastasis.
 SQ Sequence 303 BP; 83 A; 72 C; 87 G; 61 T;

Query Match 14.9%; Score 59; DB 1; Length 303;
 Best Local Similarity 56.3%; Pred. NO. 1.8e-08;
 Matches 130; Conservative 0; Mismatches 100; Indels 1; Gaps 1;

OY 10 ctggaggaaccacccatggaaggaatcatcaacatctccaccagtaactcgttcgggtggg 69
 DB 13 CTGGAGGAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAAGTACTCCGGCAAAGGGT 72
 OY 70 cattcgacacccctaaacagcgctgaagcagctgatacaaaaggaacttcccaa 129
 DB 73 GACAAGTTCAAGCTCAACAGATGATGAGCTAAAGAGCTGCTGACCC-66GAGCTGCCAG 131
 OY 130 aacctccgaacacccaagaccactacatctgacaaaatattccaagacctgagtc 189
 DB 132 CTTCCTGGGAAAGACAGATGATGAGCTCTTCCAGAGTGTGATGACCACTTGGACAG 191
 OY 190 cgataaagcggagccgctcagcttgaggaattcgtagtcctggttcag 240
 DB 192 CAACAGGACACAGAGGTGGACTTCCAGAGTACTGTGTCTTCCTCTG 242

RESULT 10
 ID T68322
 AC T68322:
 DI 16-JUL-1997 (first entry)
 DE Human multidrug resistance protein 14 (MRP14) gene.
 KW Genetic engineering; MRP; multidrug resistance protein; transgenic;
 KW animal model; cell death inhibition; apoptosis; cell proliferation;
 KW HIV; human immunodeficiency virus; cancer; cystic fibrosis; neoplasia;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT intron 1.1000
 FT /*tag= a
 FT /number= 1
 FT 871..877
 FT /*tag= b
 FT /note= "conserved DNA motif"
 FT 920..924
 FT /*tag= c
 FT /note= "conserved DNA motif"
 FT 972..977
 FT /*tag= d
 FT /note= "conserved DNA motif"
 FT 1001..1028
 FT /*tag= e
 FT /number= 1
 FT 1029..1415
 FT /*tag= f
 FT /number= 2
 FT 1029..1030
 FT /*tag= g
 FT /note= "Conserved DNA motif"
 FT 1374..1382
 FT /*tag= h
 FT /note= "conserved DNA motif"
 FT 1388..1391
 FT /*tag= i

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FT      misc_feature      /note= "conserved DNA motif"
FT      1393..1397
FT      /tag= j
FT      /note= "Conserved DNA motif"
FT      1401..1406
FT      /tag= k
FT      /note= "conserved DNA motif"
FT      1414..1416
FT      /tag= l
FT      /note= "conserved DNA motif"
FT      1417..1580
FT      /tag= m
FT      /number= 2
FT      /note= pos: 1431..1433 represents start codon"
FT      1581..3448
FT      /tag= n
FT      /number= 3
FT      1581..1582
FT      /tag= o
FT      /note= "conserved DNA motif"
FT      2738
FT      /tag= p
FT      /note= "N= a 360 nucleotide unsequenced region"
FT      3429..3440
FT      /tag= q
FT      /note= "conserved DNA motif"
FT      3447..3448
FT      /tag= r
FT      /note= "conserved DNA motif"
FT      3449..3826
FT      /tag= s
FT      /number= 3
FT      3667..3685
FT      /tag= t
FT      /note= "conserved DNA motif"
FT      3695..3706
FT      /tag= u
FT      /note= "conserved DNA motif"
FT      3708..3713
FT      /tag= v
FT      /note= "conserved DNA motif"
FT      3723..3727
FT      /tag= w
FT      /note= "conserved DNA motif"
FT      3729..3733
FT      /tag= x
FT      /note= "conserved DNA motif"
FT      3807..3812
FT      /tag= y
FT      /note= "conserved DNA motif"
FT      3827..4440
FT      /tag= z
FT      /number= 4
FT      3837..3842
FT      /tag= aa
FT      /note= "conserved DNA motif"
FT      3844..3845
FT      /tag= ab
FT      /note= "conserved DNA motif"
FT      3847..3848
FT      /tag= ac
FT      /note= "conserved DNA motif"
FT      US5614397-A.
FT      25-MAR-1997.
FT      22-FEB-1994; 200016.
FT      22-FEB-1994; US-200016.
FT      (STRD ) UNIV LEIAND STANFORD JUNIOR.
FT      Lagasse E, Weissman I;
FT      WPI; 97-224943/20.
FT      DR
FT      P-PSDB; W17062.
FT      Increasing life-span of mammalian haemato-lymphoid cells by
FT      transforming stem cells - with construct contg. cell-specific
FT      transcription initiator and gene encoding protein that increases

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PT      lifetime, useful for drug screening and treatment
PS      Example 1; Column 29-32; 34pp; English.
CC      T66322 is the human MRP14 gene. The transcriptional initiator of this
CC      gene was used in a construct for expressing an open reading frame that
CC      increase the lifespan of a mammalian haematolymphoid cell, e.g. the
CC      mammalian bcl-2 gene, a cFTR (cystic fibrosis transmembrane regulator)
CC      gene, the herpes virus thymidine kinase gene or an oncogene.
CC      Haematolymphoid cells are especially neutrophils and the construct
CC      doubles the lifespan of transgenic cells. Transgenic cells or
CC      transgenic animals produced are used for screening for substances and
CC      treatments that prevent or promote cell death. They can also be returned
CC      to the patient to modulate apoptosis, i.e. in the treatment of disorders
CC      related to abnormal cell proliferation or death. Typical applications
CC      are treatment of viral diseases, including HIV; cancer and cystic
CC      fibrosis.
SQ      Sequence 4440 BP; 1099 A; 1203 C; 1159 G; 978 T;

Query Match      14.9%; Score 58.8; DB 1; Length 4440;
Best Local Similarity 68.6%; Pred. No. 5.8e-08;
Matches 81; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Oy      1 atgactaagctggagggaccactggaggaatacacaatctccaccagtactcgtt 60
Db      1443 ATGTGCACTGGAGCGCAACATAGACACATCAACACCTCCACCAATACTCTGTG 1502
Oy      61 cgggtggggcatttcgaaccctcaacaagcgtgagctgacgacgtatcacaag 118
Db      1503 AAGCTGGGGGCAACCCAGACACCTGTGACCAAGGGGGAATTCAAGAGCTGTGCAAAAG 1560

RESULT 11
O99178
ID      O99178 standard; cDNA; 579 BP.
AC      O99178:
DE      27-DEC-1995 (first entry)
KW      Human mts-1 cDNA.
OS      Metastasis; cancer; mts-1 gene; tumour; therapy; ds.
PN      Homo sapiens.
PD      WO9520656-A1.
PE      03-AUG-1995.
PF      31-JAN-1995; U01214.
PR      31-JAN-1994; US-190560.
PA      (RESE ) RESEARCH CORP TECHNOLOGIES INC.
PI      lukandlin E, zain S;
DR      WPI; 95-275441/36.
PT      Nucleic acid encoding human mts-1, antigenic fragments and
PT      antibodies - useful for diagnosis of malignant cancer and metastatic
PT      potential of tumour cells...
PS      Claim 3; Page 93; 124pp; English.
CC      A human cDNA library was constructed in lambda-gt10 using poly(A)+
CC      RNA prepd. from HeLa cells. The library was screened with a 32P-
CC      labeled mouse mts-1 vDNA probe. A clone was obtd. which comprised
CC      the full-length human mts-1 gene (given in Q99177); 3' and 5'
CC      flanking sequences are included in the sequence of O99178. The gene
CC      can be used to express mts-1 protein, e.g. in Si21 cells, and
CC      antisense constructs are used to inhibit metastasis.
SQ      Sequence 579 BP; 130 A; 149 C; 153 G; 147 T;

Query Match      13.7%; Score 54.2; DB 1; Length 579;
Best Local Similarity 55.0%; Pred. No. 6.1e-07;
Matches 127; Conservative 0; Mismatches 103; Indels 1; Gaps 1;

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[illegible]

Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
13.1%; Score 51.6; DB 1; Length 433;	52.5%; Pred. No. 3.2e-06;	146;	0;	119;	13;	1;
Query	3	gactaagctggagagccacactggaggaatcatcaacatctccacacgacttcggtcg	62			
Db	57	gctctaactggagagagccctttaggacacccctcattgattgacacaaattatccaatt	116			
Qy	63	gctggagcatttcgagacccctcaacaagctgtagctggaagcagcgcgatcacaagaaggaac	122			
Db	117	ACAAGGAATATCCATGCGCCTCTACAAAGATATCTTCAAGAAATGGTCCATCAGAGAG	176			
Qy	123	ttcccaaaacccctcagaagacacccaagaacacccactacactgagcaaaatattccaagacc	182			
Db	177	TCCCTAGTTTGTG-----AGAAATTAATATCCAAAACCTGTTCAGAGAT	223			
Qy	183	tgtagtcgcatgaagaagcagcgcagcttggagaattctgtactctcggtgtccagag	242			
Db	224	TGGACATCATATGTGACAAATGCAATTAATCTTGAGAGAGTTCCTTGCGATGTGATTAAG	283			
Qy	243	tgctgaaaaacagccacatagatatccacaagaagtag	280			
Db	284	TGGGTGTGGCATCTCACAAAGACAGCACCAAGAGTAG	321			
RESULT	14					
ID	T68321					
AC	T68321					
DE	16-JUL-1997 (first entry)					
DE	Human multidrug resistance protein 8 (MRP8) gene.					
KM	Genetic engineering, MRP, multidrug resistance protein; transgenic;					
KM	animal model; cell death inhibition; apoptosis; cell proliferation;					
KM	HIV; human immunodeficiency virus; cancer; cystic fibrosis; neoplasia;					
KM	tumour; ss.					

Tue Mar 14 17:41:41 2000

5Q Sequence 10952 BP; 2274 A; 2850 C; 3236 G; 2592 T;

Query Match	10.6%;	Score 41.8;	DB 1;	Length 10952;
Best Local Similarity	51.5%;	Prod No 0 0087;		

Matches 67; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 10 ctgagagaccactgaggaatcatcaatcttcaccagtaactccgttcggtggg 69

D5 5961 CTGGAGAAGGCCCTGGATGTGATGTTCCACCTTCCACAAGTACTGGGCCAAGAGGGT 6020

70 catttcgacacccctcaacaagcgttgagctgagcagctgatcaaaag 118

Db 6021 GACAAGTTCAGCTCACACAAGTCAGAACTAAGGAGCTGCTGACCCGGG 6069

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Time: 1866 sec

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OM nucleic - nucleic search, using sw model

Run on: March 14, 2000, 15:45:30 ; Search time 479.61 Seconds
(without alignments)
3109.583 Million cell updates/sec

Title: US-09-167-705-1
Perfect score: 395
Sequence: 1 atgactaagctggaggaacca.....agcaaaaaaaaaaaaaaa 395

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapept 1.0

ched: 4538634 seqs, 1887831982 residues
Total number of hits satisfying chosen parameters: 9077268

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST.*

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*
44: gb_est25:*

45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_gss1:*
80: gb_gss2:*
81: gb_gss3:*
82: gb_gss4:*
83: em_gss1:*
84: em_gss2:*
85: em_gss3:*
86: em_gss4:*
87: gb_gss5:*
88: gb_gss6:*
89: gb_gss7:*
90: gb_gss8:*
91: gb_gss9:*
92: em_gss5:*
93: em_gss6:*
94: em_gss7:*
95: em_gss8:*
96: em_gss9:*
97: em_gss10:*
98: em_gss11:*
99: gb_gss10:*
100: gb_gss11:*
101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164.4	41.6	453	43	A1161013
2	164.4	41.6	466	30	AA203475

AA203475 qx55d04.r

Source	Organism	Human
Source	Homo sapiens	human.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
AUTHORS	Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
	1 (bases 1 to 417)	
	Hillier, L., Allen, M., Bowles, J., Dubuque, T., Giesel, G., Jost, S.,	
	Kitzman, D., Kucaba, M., Lacy, M., Le, N., Lennon, G., Marra, M.,	
	Matlin, J., Moore, B., Scheilenberg, K., Stepien, M., Tan, F.,	
	Thomsen, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.	
TITLE	Washington NCI human EST project	
JOURNAL	Unpublished (1997)	
COMMENT	On Sep 12, 1996 this sequence version replaced gi:1290672.	
	Contact: Wilson RK	
	Washington University School of Medicine	
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
	Tel: 314 286 1800	
	Fax: 314 286 1810	
	Email: est@wustl.wustl.edu	
	This clone is available royalty-free through LNL; contact the	
	IMAGE Consortium (info@image.lnl.gov) for further information.	
	Seq primer: -40m3 fwd. Et from Amersham.	
URES	Location/Qualifiers	
source	1. .417	
	/organism="Homo sapiens"	
	/db_xref="GDB:1335798"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:436029"	
	/clone_lib="Soares_fetal_liver_spleen_INFLS_S1"	
	/sex="male"	
	/dev_stage="20 week-post conception fetus"	
	/lab_host="DH10B (ampicillin resistant)"	
	/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia	
	with a modified polylinker; Site_1: Pac I; Site_2: Eco RI	
	This is a subtracted version of the original Soares fetal	
	liver spleen INFLS library. 1st strand cDNA was primed	
	with a Pac I - oligo(dT) primer [5],	
	AACGAGAGATTAATTAACATCTTTTCTTTTCTTTT 3']	
	double-stranded cDNA was ligated to Eco RI adaptors	
	(Pharmacia), digested with Pac I and cloned into the Pac I	
	and Eco RI sites of the modified pT73D vector. Library	
	went through one round of normalization. Library	
	constructed by Bento Soares and M.Fatima Bonaldo."	
BASE COUNT	101 a 93 c 97 g 126 t	
ORIGIN		
Query Match	40.8%; Score 161.2; DB 37; Length 417;	
Best Local Similarity	75.5%; Pred No. 9.6e-35;	
Matches 213; Conservative	0; Mismatches 68; Indels 1; Gaps 1	
1	atgactaagctgagagaccctgagaggaatcatcatcattccacacagctactccgt 60	
Db	391 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTCATATCTTCACCAATATCAGT 332	
0Y	61 cgggtgggggcatctcgacacccctcaacaagcgtgagctgagcagcgtgatacaaaaggga 120	
Db	331 CGGAAGGGGCAATTTGACACCCCTCTCTAAGGGGTGGGCTCAACAGCTGCTTCAAA-TGA 273	
0Y	121 acttccaaacccctccagaacaacaagaacaaacctaccattggaataaatttccaaga 180	
Db	272 GCTTCACAAACCATCAACAAATATCAAAATTAAGCTGTCAATGATGAATATATCCAAAG 213	
0Y	181 cctgtagtcgcgaataaagagagcgcctgacgtcttgaggaattcgtatgctgctgcag 240	
Db	212 CCGTGAATGATATCAAGATGAACAGTGCACATTTTCAAGATTCATATCCCTGTACCAT 153	
0Y	241 ggtgctgaaacacagccacatagatatccacaagaagatgagt 282	
Db	152 TCGCGTGAAGGCTGCCCATTTACACACCAACCAAGAGTAGT 111	
RESULT	5	
	W65311	

LOCUS			65311	439 bp	mRNA	EST	15-OCT-1996
DEFINITION			Z33J02.R1 Soares_fetal_heart_NDHL19W homo sapiens cDNA clone IMAGE:342458 5' similar to SW:CAGC_PIG P80310 CALGRANULIN C ; , mRNA sequence.				
ACCESSION			W65311				
VERSION			W65311.1	GI:1373637			
KEYWORDS			human.				
SOURCE			Homo sapiens				
ORGANISM			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE			1 (bases 1 to 439)				
AUTHORS			Haller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Parsons,O., Rifkin,L., Romling,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.				
TITLE			The WashU-Merck EST Project				
JOURNAL			Unpublished (1995)				
COMMENT			On Apr 14, 1993 this sequence version replaced gi:692790. Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 1367 Std Error: 0.00 Seq primer: mob.REGA+EV. Location/Qualifiers 1..439 /organism="Homo sapiens" /db_xref="GDB:1267833" /db_xref="taxon:9606" /clone="IMAGE:342458" /clone_lid="Soares_fetal_heart_NDHL19W" /sec="unknown" /dev_stage="19 weeks" /lab_host="DH10B (ampicillin resistant)" /note="Organ: heart; Vector: pTVT3D (Pharmacia) with a modified polylinker; Site.1: Not I ; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATCTGAAGTCGGCGGCCGCATCTTTTTTTTTTTT 3'] , double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTVT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Patrina Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NDHL19W."				
FEATURES							
SOURCE							
BASE COUNT			126 a	105 c	101 g	105 t	2 others
ORIGIN			NBDHL19W,"				
Query Match			Best Local Similarity	39.2%	Score 155;	DB 26;	Length 439;
Matches 216;			Conservative	0;	Mismatches 65;	Indels 2;	Gaps 2;
OY			1 atgactaaagctggaggaccaccccttggaaggaatatcaaatcattccacagtagtacctgtt	60			
Dd			64 ATGACAAAACCTTGAAAGACCATCTGGAGGGAATTGTCAATAATCTCCACCAAATACCAACTT	123			
OY			61 cgagtggggcatlttcgaacacctcaacaagaagcgtagtcgtgaagcaagctgatcacaaaagga	120			
Dd			124 CGAAGGGGCGATTGTGARACCCCTCTCTTAAGGTTAGTCGTGAAGCACACCTCTTACAAG	182			
OY			121 acttcccacaaacctccgaacaaccaagaagaccacctaaccattgacaaaaataattccaaga	180			
Dd			183 GCTTCCAACACACCATCAAGAATATCAAGAAATAAACCTGTCAATTGTGTAATAATTCCAAGG	242			
OY			181 ccctgatgcgcataaagcgcga-ggccgcacagctttgaggaatttgttaacctgtgtgtcca	239			

QY	240	99gfgctga	aaacagccacatagatatccacaaggtaggt	282
Db	243	CCTGATGCTCTATCATCAAGTGAACACGGTCGAGATCTTCAGGAATTCATATCCCTGGTAGCCA	302	
RESULT	6			
LOCUS	AA707079/c			
DEFINITION	AA707079	286 bp	mRNA	EST
VERSION	AA707079.1	GI:2716997		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
AUTHORS	Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	1 (bases 1 to 286)			
	Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gaisel, G., Jost, S.,			
	Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,			
	Martin, J., Moore, B., Schellenberg, K., Stepec, H., Tan, F.,			
	Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.			
	WashU-NCI human EST project			
	Unpublished (1997)			
COMMENT	On Dec 18, 1997 this sequence version replaced gi:23400250.			

```

Email: est@station.wustl.edu
This clone is available royalty-free through LINT ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amer sham.
Location/Qualifiers
1..286
FEATURES
source

```

```

/organism="Homo sapiens"
/db_xref="GDB:1387950"
/db_xref="taxon:9606"
/clone_image="451594"
/clone_lib="Soares_fetal_liver_spleen_JNFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: Liver and Spleen; Vector: pT73D (Pharmacia) with a modified polylinker; Site.1: Pac I; Site.2: Eco RI. This is a subtracted version of the original Soares fetal liver spleen JNFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACGCGAAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

```

Query Match	38.6%	Score 152.4	DB 37	Length 286
Best Local Similarity	75.2%	Pred. No. 2.4e-32		
Matches	203	Conservative	0	Mismatches 66; Indels 1; Gaps 1;
Oy	1	atgactaagcttggagaccaccttggaggaatcattcaacaatcttcacacgaagtccgt	60	
Db	269	ATGCAAAACTTGAGAGACATCTGGAGGGAATTGCAATATCTTCCACCAATACGAGT	210	
Oy	61	cgagtcggggcatttcgacacccctcaacaagcttggcttgaagaacagctctatcaagaagga	120	

Db 209 CGGAAGGGGCAATTTTGACACCCTCTAAAGGTGAGCTGAAGCAGCTGTTACAA- GGA 151
 QY 121 acttcccaaaacccctccagaacaccaaagaccacttaccatgacacaaatattccaaga 160
 Db 150 GCTTGCACAAACCCATCAAGAAATATCAAAAGATAAAGGCTGATATGNTAAATATTCCAAG 91
 QY 181 cctgatgctcgataaagaacgagagcgcacagttagtgagaattctgacctggtgtccag 240
 Db 90 CCTGGAATCTTAATGAAGTGAACAGGTGACACTTTCAGAAATCATATCCCTGGTAGCCAT 31
 QY 241 ggtgctgaaacagccacacatagaatacca 270
 Db 30 TGCGGTGAAGGCTGCCCATTTACCAACCA 1

	RESULT	7	
AA313230			
LOCUS	AA313230	311 bp	mRNA
DEFINITION	EST18532 Liver, subtracted (abundant clones) II Homo sapiens cDNA		19-APR-1997
ACCESSION	AA313230		
VERSION	AA313230.1		
KEYWORDS	GI:1965761		
SOURCE	EST.		
ORGANISM	human.		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
	Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
REFERENCE	1 (bases 1 to 311)		
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,		

Balle,C.J., Sutton,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D.,
 White,O.J., Lee,N.G., Blake,J.C., Brandon,R.C., Man-
 Mait,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geopghagen,N.S.,
 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
 Kelley,U.M., Kelley,J.C., Liu,L.-I., Mammos,S.M., Merrick,J.M.,
 Moreno-Palancques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,
 Small,K.V., Spilgys,T.A., Utterback,T.R., Weidman,J.F., Wil-
 Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dimke,D., Feng,D.-F., Fertie,A., Fischer,C., Hastings,G.A.,
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H.,
 Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M.,
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
 Fraser,C.M., and Venter,J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl), 3-174 (1995)

Other_ESTs: THC189199
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699036
Tel: 3018699423
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES	SOURCE	LOCATION/Qualifiers
	1..311	
	/organism="Homo sapiens"	
	/db_xref="ARCC (inhost):117150"	
	/db_xref="taxon:9606"	
	/clone_lib="liver, subcloned (abundant clones) II"	
	/dev_stage="adult"	
	/note="Organ: liver; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"	
BASE COUNT	93 a	79 t
ORIGIN	67 c	79 g
		2 others

FEATURES
Seq primer: M13 Reverse.
Location/Qualifiers
Source 1..284

/organism="Homo sapiens"
/db_xref="ATCC (Inhost):121788"
/db_xref="taxon:9606"
/clone_id="Bone marrow"
/sex="mixed"
/tissue_type="bone marrow"
/dex_stage="adult"
/note="Vector: pluescript SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 89 a 57 c 65 g 71 t 2 others
ORIGIN

Query Match 35.4%; Score 140; DB 31; Length 284;
Best Local Similarity 77.4%; Pred. No. 6.8e-29;
Matches 181; Conservative 0; Mismatches 52; Indels 1; Gaps 1;

OY 1 atgactaagctggagagaccacgtgaggaatcatcaacattctccacagctcgtt 60
Db 50 ATGACAAACTGGAAGACATCTGGAGGAATTCATATCTTCACCAATCTCAGTT 109
OY 61 cgggtgggacatttcgacacacctcaacaagcgtgagctgaagcagctga:cacaaggga 120
Db 110 CGGAAGGGGCAATTTCAGACCCCTCTTAAGGTGAGCTGAAGCAGCTGCTTCAAA-GGA 168
OY 121 acttcccaaaacctccgagacacccaagacacacctaccattgcaaaatattccaaga 180
Db 169 GCTTCGAACACCATCAAGAAATATCAAGATTAACCTGTCATTGATGAATATTCGAAG 228
OY 181 cctgataccgataaagacgagcgctgacgttgaaggaattcgagtcgt 234
Db 229 CCTGNTCTATCATCAAGATGAACAGCTGACCTTCAGATTCATATCCCTGGT 282

RESULT 10
LOCUS AI1365228 374 bp mRNA EST 16-FEB-1999
DEFINITION q241b12.x1 NCI-CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2029439 3'
VERSION AI1365228
ACCESSION AI1365228.1 GI:4124917
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 374)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 19, 1998 this sequence version replaced gi:2152886.
CONTACT: Robert Strausberg, Ph.D.
Tel: (301) 486-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html

FEATURES
Seq primer: -40bp from Gibco
High quality sequence stop: 245.
Location/Qualifiers
Source 1..374
/organism="Homo sapiens"

/db_xref="taxon:9606"
/clone="IMAGE:2029439"
/clone_id="NCI CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: p7T73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI-CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT 92 a 74 c 91 g 117 t
ORIGIN

Query Match 35.3%; Score 139.6; DB 45; Length 374;
Best Local Similarity 75.6%; Pred. No. 9.5e-29;
Matches 186; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

OY 37 aacatctccacagctactcgttcgtggtgggaattcgacacctcaacaagcgtgag 96
Db 374 AATATCTTCACCAATATCTCAGTTTCGGAAGGGCATTTGACCCCTCTTAAGGTTGAG 315
OY 97 ctgaagcagctgatacaaaagggaacttcccaaacctccagaacaccagaaccacc 156
Db 314 CTGAAGCAGCTGCTTACAA-GGAGCTTGCAAAACCCATCAAGAAATATCAAGATTAAGC 256
OY 157 taccattgcaaaatattccaagaacctgtagccgataaagcagcgtcagcttga 216
Db 255 TGTCATTATGAATATTCACCAAGGCTGATGCTTAATGAATGAACGATGCTTCA 196
OY 217 ggaattcgtactcctggtgctcaggggtcgtgaagcagccacatagatccacaaga 276
Db 195 AGAATTCATATCCCTGATGAGCATTGCGCTGAAGGCTCCCATTAACACACCACAAAGA 136
OY 277 gtaggt 282
Db 135 GTAGGT 130

RESULT 11
LOCUS AI863618 395 bp mRNA EST 30-AUG-1999
DEFINITION wh73c02.x1 NCI-CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2386370 3'
VERSION AI863618
ACCESSION AI863618.1 GI:5527725
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 395)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Dec 20, 1995 this sequence version replaced gi:1136060.
CONTACT: Robert Strausberg, Ph.D.
Tel: (301) 486-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html

Oy	95	aaccctgaagcagtcgttcccaaaagggaacttcccacaaacctccaagaacccaagacca	154
Dd	321	AGATGACAGCAGCTGCTTACAAG-GGAAGCTTGCAAAACACCATCATAGAATTTCAAAGATAA	263
Oy	155	cctaccatgacaaaataattccaaagacctgtagtgcgatataaagacggagcgctcagtt	214
Dd	262	GCTGTCAATTGATGAATAATATTCACAGGCCCGTAGTGCATTAACAGATGAACAGAGCTT	203
Oy	215	ggaggaatcgtatgctgtcgtgcagggtgcctggaacaacgcccatatgatatcacaaa	274
Dd	202	CAGAAATTCATATCCCTGGTAGCAATTCGGCGTGAAGGCTGCCCATTTACCAACACCAAAA	143
Oy	275	gagtagtg 282 	
Dd	142	GAGTAGGT 135	
RESULT	15		
LOCUS	R02721	458 bp mRNA EST 31-MAR-1995	
DEFINITION	Yer6a09..r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:123640 5' similar to SP:CAC_C_PIG P80310 CALGRANDLIN C ; , mRNA sequence.		
ACCESSION	R02721		
VERSION	R02721.1	GI:752457	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 458) Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hillman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.		
TITLE	The MashU-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 518 This high quality sequence stops: 224 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 518 Std Error: 0.00 Seq primer: M13RP1 High quality sequence stop: 224. Location/Qualifiers 1..458 /organism="Homo sapiens" /db_xref="GDB:476185" /db_xref="taxon:9606" /clone="IMAGE:123640" /clone_lib="Soares fetal liver spleen INFLS" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" /note="Organ: Liver and Spleen; Vector: pTZ19 (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'] , double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTZ19 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fátima Bonalido."		
BASE COUNT	116 a 109 c 108 g 120 t 5 others		
ORIGIN			

Query Match	29.0%	Score 114.4	DB 21	Length 458
Best Local Similarity	71.2%	Pred. No. 1e-21		
Matches 151	Conservative 0	Mismatches 61	Indels 0	Gaps 0
Qy	1 atgactaagctgagagaccacctgtaggagaaatcaatcatcttcaccagtaactcgtt	60		
Db	ATGACAAAACCTTGAAGAGCATCTGGAGGGAAATTGTCATATCTTCCACCAATACGATT	112		
Qy	61 cggagtgaggagcatttagaacacctcaacaagcttgagcctgaaacagatcatccaaagga	120		
Db	113 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGTGAGCTGAGACACTGCTTTCAAAGGAG	172		
Qy	121 acttcccaaaacctccagaaacccaacaaagacaaactcaatctgaacaataattccaaga	180		
Db	173 CTTGCAAAACACCATCAAGAAATATCAAAAGATMAACCTGATTCATGGATGAATATTCGAAG	232		
Qy	181 cctgatagcagataaagagcgagccgtgaact	212		
Db	233 CTTGGGAGTGCCTTAATCAAGGATGGAACAGGT	264		

Search completed: March 14, 2000, 16:13:06
Job time: 1656 sec

Page 10

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 14, 2000, 15:37:00 ; Search time 12.36 Seconds
(without alignments)
95.818 Million cell updates/sec

Title: US-09-167-705-2

Perfect score: 259
Sequence: 1 TKLEPDHEGIIINIGHOYSVR.....ELKQLGTRKELPKTLQNKDKQ 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 168963

Minimum DB seq length: 0
Maximum DB seq length: 1000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	88.8	92	1 W03563	Calcium binding pr
2	206	79.5	91	1 W01826	Component of bioac
3	206	79.5	91	1 W93819	Angiotropin relate
4	189	73.0	92	1 W03564	Calcium binding pr
5	189	73.0	92	1 W24137	Human chemotacti
6	139	53.7	30	1 R85169	Bovine serum hepar
7	110	42.5	114	1 W17062	Human multitrug re
8	110	42.5	114	1 W60178	Human calprotectin
9	83	32.0	91	1 W46607	Human brain protei
10	83	32.0	101	1 R20560	Human mts protein
11	83	32.0	101	1 R80453	Human mts-1 protei
12	74	28.6	66	1 P50052	Sequence of human
13	74	28.6	93	1 W17061	Human multitrug re
14	74	28.6	93	1 W60177	Human calprotectin
15	73	28.2	89	1 R22429	Human CP-10. New
16	68	26.3	98	1 W27152	Human chemotacti
17	68	26.3	98	1 W82409	Human S100P2 prote
18	67	25.9	97	1 R26406	Sequence of the cl
19	67	25.9	97	1 R27058	Sequence of small
20	66	25.5	38	1 W46608	Human brain protei
21	58.5	22.6	876	1 W59032	B. pallidus DNA po
22	58.5	22.6	1276	1 W59034	B. pallidus DNA po
23	58	22.4	33	1 W46610	Human brain protei
24	57	22.0	26	1 R49434	Calgranulin B post
25	55	21.2	24	1 R49435	Calgranulin B post
26	55	21.2	3001	1 W19692	ATM mutant 4612del
27	55	21.2	3001	1 W19670	ATM mutant 4612del
28	54.5	21.0	501	1 R27741	Sequence transcrib
29	53	20.5	3722	1 R10145	Cephalosporin anti
30	51.5	19.9	76	1 W75703	Calcium binding pr
31	51.5	19.9	165	1 Y11071	H. pylori ORF 099e
32	51.5	19.9	213	1 W11072	H. pylori ORF hp2p
33	51.5	19.9	789	1 W14055	Pumpkin ent-kauren
34	50.5	19.5	748	1 W13384	Human protein ubiq

35	50.5	19.5	1084	1 W59033	B. pallidus DNA po
36	50	19.3	208	1 W89231	Mouse osteoprotege
37	50	19.3	401	1 W38344	Mouse osteoprotege
38	50	19.3	540	1 R72678	Protein deduced fr
39	49.5	19.1	120	1 W78465	S. aureus grea prot
40	49.5	19.1	3685	1 P90290	Human Duchenne mus
41	49	18.9	344	1 W98545	H. pylori GHPO 156
42	49	18.9	513	1 W79755	Euphorbia lagascae
43	48.5	18.7	344	1 W20917	H. pylori cell env
44	48.5	18.7	344	1 W55362	H. pylori ORF 149p
45	48.5	18.7	447	1 W20510	H. pylori inner me

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB ID	Description
1	W03563	230	88.8	92	1 W03563	Calcium binding pr
2	W01826	206	79.5	91	1 W01826	Component of bioac
3	W93819	206	79.5	91	1 W93819	Angiotropin relate
4	W03564	189	73.0	92	1 W03564	Calcium binding pr
5	W24137	189	73.0	92	1 W24137	Human chemotacti
6	R85169	139	53.7	30	1 R85169	Bovine serum hepar
7	W17062	110	42.5	114	1 W17062	Human multitrug re
8	W60178	110	42.5	114	1 W60178	Human calprotectin
9	W46607	83	32.0	91	1 W46607	Human brain protei
10	R20560	83	32.0	101	1 R20560	Human mts protein
11	R80453	83	32.0	101	1 R80453	Human mts-1 protei
12	P50052	74	28.6	66	1 P50052	Sequence of human
13	W17061	74	28.6	93	1 W17061	Human multitrug re
14	W60177	74	28.6	93	1 W60177	Human calprotectin
15	R22429	73	28.2	89	1 R22429	Human CP-10. New
16	W27152	68	26.3	98	1 W27152	Human chemotacti
17	W82409	68	26.3	98	1 W82409	Human S100P2 prote
18	R26406	67	25.9	97	1 R26406	Sequence of the cl
19	R27058	67	25.9	97	1 R27058	Sequence of small
20	W46608	66	25.5	38	1 W46608	Human brain protei
21	W59032	58.5	22.6	876	1 W59032	B. pallidus DNA po
22	W59034	58.5	22.6	1276	1 W59034	B. pallidus DNA po
23	W46610	58	22.4	33	1 W46610	Human brain protei
24	R49434	57	22.0	26	1 R49434	Calgranulin B post
25	R49435	55	21.2	24	1 R49435	Calgranulin B post
26	W19692	55	21.2	3001	1 W19692	ATM mutant 4612del
27	W19670	55	21.2	3001	1 W19670	ATM mutant 4612del
28	R27741	54.5	21.0	501	1 R27741	Sequence transcrib
29	R10145	53	20.5	3722	1 R10145	Cephalosporin anti
30	W75703	51.5	19.9	76	1 W75703	Calcium binding pr
31	Y11071	51.5	19.9	165	1 Y11071	H. pylori ORF 099e
32	W11072	51.5	19.9	213	1 W11072	H. pylori ORF hp2p
33	W14055	51.5	19.9	789	1 W14055	Pumpkin ent-kauren
34	W13384	50.5	19.5	748	1 W13384	Human protein ubiq

KM angiogenesis; vascular state; mammalian tissue; transfer; cell;
 KM genetic information; selective; alteration; nucleic acid content;
 KM leukocyte; pig; monocytic-CuRNP.
 OS Sue scrofa.
 PN DE19628895-A1.
 PD 23-JAN-1997.
 PF 17-JUL-1996; 028895.
 PR 18-AUG-1995; DE-030500.
 PR 17-JUL-1995; DE-025992.
 PA (FRAU) FRAUNHOFER GES FORDERUNG ANGENANDTEN.
 PI Hellmeyer IMG, Kieseletter S, Logemann E, Wissler JH;
 DR WPI: 97-088586/09.
 DR N-PSDB; T62569.
 PT Bioactive metal RNA polypeptide - useful for modulating
 PT angiogenesis, etc.
 PS Claim 1; Page 15; 16pp; German.
 CC A novel bioactive metal RNA polypeptide (RNP) has a RNA component
 including the sequence T62568 and a polypeptide component having
 the sequence W01826, which is encoded by T62569. The RNP, or
 anti-RNP immunoglobulins, can be used to modulate and/or analyse
 angiogenesis and the vascular state of mammalian tissue, transfer
 genetic information in cells and selectively alter the nucleic
 acid content of cells.
 CC Leukocytes from pig's blood were cultured in medium, and the
 supernatant treated with NH₄ sulphate at 35, 45 and 90% saturation
 to precipitate protein fractions. The residual supernatant was
 diluted to 45% NH₄ sulphate saturation and concentrated by
 ultrafiltration using a 0.5 kD membrane. The retentate was purified
 to give 8 mg of product described as monocytic-CuRNP.
 SQ Sequence 91 AA;

Query Match 79.5%; Score 206; DB 1; Length 91;
 Best Local Similarity 82.0%; Pred. No. 2.1e-22;
 Matches 41; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 TKLEDHLEGIINIGHQSVRGHFDTLNKYELKOLGTRELPKTLONKXKDQ 50
 |||||
 DB 1 TKLEDHLEGIINIGHQSVRGHFDTLNKYELKOLGTRELPKTLONKXKDQ 50

RESULT 3

ID W93819 standard; peptide; 91 AA.

AC W93819;

DT 21-JUN-1999 (first entry)

DE Angiotropin related protein; ARP; ternary complex; S100 protein;

KM copper-containing ribonucleoprotein; copper; cell selective;

CC morphogenic action; blood capillary endothelial cell; confluent;

CC non-mitogenic induction; cell phenotype; three-dimensional organoid;

KM spatiotemporal supracellular organisation; chemotrophic; blood vessel;

KM tissue neovascularisation; angiogenesis modulation.

OS Synthetic.

PN DE19811047-C1.

PD 15-APR-1999.

PR 13-MAR-1998; 011047.

PR 13-MAR-1998; DE-011047.

PA (FRAU) FRAUNHOFER GES FORDERUNG ANGENANDTEN.

PI Brunner H, Kieseletter S, Koch-Palster B, Kuhn E;

DR WPI: 99-216114/19.

PT Copper-containing ribonucleoproteins - useful for modulating

PT angiogenesis

PS Disclosure; Page 2; 16pp; German.

CC This invention describes novel copper-containing ribonucleoproteins

CC which are ternary complexes of an S100 protein, copper ions, and

CC RNA comprising the following consensus sequence or its complement

CC GGAAGAUNNNUNNACUGN1-6CUNNUNNUNNNNAAAANO-10ANAACAUNO-5CUNNAGNO-

CC 13AGAA-AUNO-16UAGAG where N = G, A, U or C. The ribonucleoproteins are

CC stated to have the following properties (1) cell-selective morphogenic

CC action in vitro on isolated primary and/or cloned blood capillary

CC endothelial cells in culture for the non-mitogenic induction of the

CC change in cell phenotype from the confluent state, for non-mitogenic

CC alteration of the spatiotemporal supracellular organisation of cells
 CC into three-dimensional organoid, capillary-like structures in culture,
 CC (2) a specific chemotrophic action on blood vessels in vivo, (3) induction
 CC of directional growth of blood vessels in vivo and (4) induction of
 CC neovascularisation of tissues through directed ingrowth of blood vessels.
 CC Their use for modulating angiogenesis is claimed.
 SQ Sequence 91 AA;

Query Match 79.5%; Score 206; DB 1; Length 91;
 Best Local Similarity 82.0%; Pred. No. 2.1e-22;
 Matches 41; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 TKLEDHLEGIINIGHQSVRGHFDTLNKYELKOLGTRELPKTLONKXKDQ 50
 |||||
 DB 1 TKLEDHLEGIINIGHQSVRGHFDTLNKYELKOLGTRELPKTLONKXKDQ 50

RESULT 4

ID W03564 standard; Protein; 92 AA.

AC W03564;

DT 01-MAY-1997 (first entry)

DE Calcium binding protein CAAFI.

KM Calcium binding protein; human; amniotic fluid; S100 protein family;

KM Intracellular signal transduction; squamous epithelial cell; neutrophil;

KM macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;

KM squamous cell carcinoma; skin; oesophagus; CAAFI; lung; blood disease.

OS Homo sapiens.

PN EP-731166-A2.

PD 11-SEP-1996.

PF 04-DEC-1995; 119045.

PR 06-MAR-1995; JP-070468.

PR 06-MAR-1995; JP-045564.

PA (HITO/) HITOMI J.

PA (TOFU) TONEN CORP.

PI Hitomi J, Kimura T, Yamaguchi K, Yamamura T;

DR WPI: 96-403989/41.

DR N-PSDB; T39346.

PT New human or bovine calcium binding protein and related nucleic acid

PT - is a marker for inflammation, neoplasia, skin and blood diseases

PS Claim 1; Page 24; 36pp; English.

CC This sequence represents the CAAFI calcium-binding protein isolated from

CC human amniotic fluid. CAAFI belongs to the S100 protein family, which

CC includes calyculin, MRP8, and MRP14. Intracellular calcium ion

CC concentration is one of the key factors for intracellular signal

CC transduction. The calcium signals are transduced by various

CC calcium-binding proteins, such as this protein. CAAFI is normally

CC expressed in squamous epithelial cells, neutrophils and macrophages, but

CC atypical epithelial cells are negative for CAAFI and overexpression is

CC observed in several types of cancer cells and neutrophils/macrophages

CC infiltrating cancerous lesions. Detection of CAAFI (using antibodies in

CC usual immunassays) can be used to diagnose (or monitor) inflammation,

CC neoplasia (particularly squamous cell carcinoma of the skin, oesophagus,

CC lung and cervix), and skin and blood diseases.

SQ Sequence 92 AA;

Query Match 73.0%; Score 189; DB 1; Length 92;
 Best Local Similarity 74.0%; Pred. No. 5.7e-20;
 Matches 37; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 TKLEDHLEGIINIGHQSVRGHFDTLNKYELKOLGTRELPKTLONKXKDQ 50
 |||||
 DB 2 TKLEDHLEGIINIGHQSVRGHFDTLNKYELKOLGTRELPKTLONKXKDQ 51

RESULT 5

ID W24137 standard; Protein; 92 AA.

AC W24137;

DT 28-JAN-1998 (first entry)

DE Human chemotactic cytokine I.

RESULT	7
W17062	
ID	W17062 standard; Protein; 114 AA
AC	W17062;
DT	16-JUL-1997 (first entry)

PR Inhibiting kidney stone formation - uses the protein calprotectin
 PT Example 1: Columns 21-22; 19pp; English.
 CC This represents a human calprotectin subunit MRP-14. This is used in
 CC a method for inhibiting the formation of a mineral precipitate in a
 CC solution, which comprises providing a solution comprising component ions
 CC of the mineral precipitate or its precursors and contacting the solution
 CC with an effective amount of isolated calprotectin, or a derivative of it.
 CC The method is useful for the inhibition of kidney stone formation (renal
 CC calculi). Kidney stones are concentrations of inorganic and organic salts
 CC that develop through crystal nucleation, aggregation and growth in the
 CC kidneys, which then can block the ureter and if not passed to the

CC bladder, grow and become symptomatic. Struvite stones (MgNH₄PO₄) are
 CC commonly found after urinary tract infection. The mechanisms of this and
 CC other stone formation is unclear, but some urine compositions are known
 CC to inhibit formation. One of the major components of these is a protein
 CC factor calprotectin, which inhibits mineral precipitation. Calprotectin
 CC can also be used to raise antibodies, which in turn can be used to detect
 CC the protein in samples. The levels of calprotectin found in samples can
 CC be compared to levels found in normal humans, and thus assuming increased
 CC calprotectin correlates to indication of kidney stone formation, this
 CC procedure can be used as a diagnostic tool.
 SQ Sequence 114 AA;

Query Match 42.5%; Score 110; DB 1; Length 114;
 Best Local Similarity 51.1%; Pred. No. 1.6e-08;
 Matches 23; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

OY 1 TRKEDHLEGINIGHOYSVRVGHFDLTKKELQGLTKELPKLQ 45
 DB 6 SQERNETITNTFHQYSVRLGHFDLTKKELQGLTKELPKLQ 50

W46607
 ID W46607 standard; protein; 91 AA.
 AC W46607;
 DT 01-JUL-1998 (first entry)
 DE Human brain protein S100b beta subunit.
 KW Human brain protein S100b; cerebral; neural; antibody;
 KW Immunological assay; diagnosis; cerebral dysfunction;
 KW melanoma cancer.
 OS Homo sapiens.
 PN WO9801471-A1.
 PD 15-JAN-1998.
 PF 27-JUN-1997; SE1164.
 PR 05-JUL-1996; SF-002677.
 PA (SANG-) SANGTEC MEDICAL AB.
 PI Brundell J, Nyberg L;
 DR WPI; 98-100999/09.
 PT Peptide(s) from human brain protein S100b beta fragments useful in
 PT S100 assay - by producing antibodies directed to the peptide(s),
 PT useful e.g. for diagnosis and monitoring of cerebral dysfunction and
 PT melanoma cancer.
 PS Disclosure; Page 18-19; 29pp; English.
 CC The Human brain protein S100b is known to be one of a number of soluble
 CC small molecule weight proteins which are released into the cerebral
 CC extracellular fluid due to cellular disruption of nervous tissue and
 CC cells of neural origin. The beta subunit of the protein has been used
 CC to produce epitopes (W46608-W46614) and corresponding antibodies which
 CC can be used in immunological assay methods. Determining the presence of
 CC brain protein S100b allows diagnosis and monitoring of patients with
 CC cerebral dysfunction and melanoma cancer.
 SQ Sequence 91 AA;

Query Match 32.0%; Score 83; DB 1; Length 91;
 Best Local Similarity 40.0%; Pred. No. 8.6e-05;
 Matches 20; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

OY 1 TRKEDHLEGINIGHOYSVRVGHFDLTKKELQGLTKELPKLQ 50
 DB 1 SELEKAVVALIDVHFQYSGREGDKHKLKSELKELINNELSHLEIKQ 50

RESULT 10
 R20560
 ID R20560 standard; protein; 101 AA.
 AC R20560;
 DT 14-MAY-1992 (first entry)
 DE Human mts protein.
 KW Metastatic cancer; antibodies; mouse; lung; liver; kidney; thyroid;
 KW breast cancer; cell growth.
 OS Homo sapiens.

FH Key Location/Qualifiers
 FT protein 1..101
 FT /label= mts-1
 FT peptide 2..11
 FT /note= "antigenic"
 FT peptide 22..37
 FT /note= "antigenic; calcium binding domain"
 FT peptide 42..54
 FT /note= "antigenic"
 FT peptide 87..101
 FT /note= "antigenic"

PN WO9200757-A.
 PD 23-JAN-1992.
 PR 09-JUL-1991; U04832.
 PF 09-JUL-1990; US-550600.
 PA (RESE) RES CORP TECHN INC.
 PI Zain S, Lukandin E;
 DR WPI; 92-056647/07.
 DR N-PSDB; Q20506.
 PT Metastatic cancer diagnosis by detection of mts-1 gene or protein
 PT - using antibody treatment of cancer and tumours of e.g. kidney,
 PT thyroid, lung and liver
 PS Claim 9; Fig 2; 82pp; English.
 CC The sequence was deduced from the DNA sequence obtd. by screening a
 CC human cDNA library with mouse mts-1 cDNA probes. The antigenic
 CC mts-1 peptides (see features) derived from the protein and anti-
 CC bodies raised to them are useful in the diagnosis of metastatic
 CC cancer, e.g. lung, kidney, thyroid or breast cancer. The peptide
 CC comprising the calcium binding site generates antibodies reactive
 CC with many members of the calcium binding protein family; the other
 CC three peptides are unique to mts-1 and generate antibodies specific
 CC only for this protein. Cell lines capable of expressing mts-1 are
 CC useful as model systems for in vitro and in vivo anti-metastasis
 CC drug screening. Pharmaceutical compns. conty. the mts-1 protein or
 CC anti-cancer reagents may be used to promote cell growth, or for
 CC treating cancer, respectively.
 SQ Sequence 101 AA;

Query Match 32.0%; Score 83; DB 1; Length 101;
 Best Local Similarity 41.7%; Pred. No. 9.8e-05;
 Matches 20; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

OY 3 LEDHLEGINIGHOYSVRVGHFDLTKKELQGLTKELPKLQ 50
 DB 5 LKRALDVWSTFHKYSKRGDKFKLKLKSELKELRLRELPFGKRTDE 52

RESULT 11
 R80453
 ID R80453 standard; protein; 101 AA.
 AC R80453;
 DT 27-DEC-1995 (first entry)
 DE Human mts-1 protein.
 KW Metastasis; cancer; mts-1 gene; tumour; therapy.
 OS Homo sapiens.
 PN WO9520656-A1.
 PD 03-AUG-1995.
 PF 31-JAN-1995; U01214.
 PR 31-JAN-1994; US-190560.
 PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
 PI Lukandin E, Zain S;
 DR WPI; 95-275441/36.
 DR N-PSDB; Q99177.
 PT Nucleic acid encoding human mts-1, antigenic fragments and
 PT antibodies - useful for diagnosis of malignant cancer and metastatic
 PT potential of tumour cells.
 PS Claim 12; Page 92; 124pp; English.
 CC A human cDNA library was constructed in lambda-gt10 using poly(A)+
 CC RNA prepd. from HeLa cells. The library was screened with a 32p-
 CC labeled mouse mts-1 cDNA probe. A clone was obtd. which comprised
 CC the full-length human mts-1 gene. The encoded protein is used for
 CC the diagnosis or therapy of cancer, and to raise antibodies.

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OM protein - protein search, using SW model

Run on: March 14, 2000, 15:37:00 ; Search time 13.75 Seconds
(without alignments)
171.525 Million cell updates/sec

Title: US-09-167-705-2

Perfect score: 259
Sequence: 1 TKLEDEHLEGIINIGHQYSVR.....ELKQLGTEKLPKTLQNXKQD 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR-62:*

1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	79.5	91	2	A55406 calgranulin c - pi
2	189	73.0	92	2	JC4712 S-100 calcium-bind
3	131	50.6	122	1	A42628 calgranulin B - bo
4	114	44.0	113	1	UN0686 calgranulin B - ra
5	110	42.5	114	1	B31848 calgranulin B - hu
6	89	34.4	101	2	S06207 calvasculin - mous
7	87	33.6	95	2	S24146 S-100 protein P -
8	87	33.6	101	2	S01759 calvasculin - rat
9	84	32.4	92	1	BCHURB S-100 protein beta
10	84	32.4	92	2	A26557 S-100 protein beta
11	84	32.4	92	2	A48015 S-100 protein beta
12	83	32.0	91	1	BCBO1B S-100 protein beta
13	83	32.0	100	2	A53217 placental calcium-
14	83	32.0	101	2	A48219 calvasculin - huma
15	81	31.3	591	2	A45135 profilaggrin - hum
16	78	30.1	113	1	S68242 calgranulin B - mo
17	77	29.7	306	1	major epidermal ca
18	74	28.6	93	1	BCHUCF calgranulin A - hu
19	73	28.2	89	1	I56163 calgranulin A - mo
20	72	27.8	95	1	S35985 S-100 protein alph
21	71	27.4	94	1	BCHURA S-100 protein alph
22	71	27.4	94	1	BCBO1A calgranulin A - ra
23	70	27.0	89	1	UN0685 S-100 calcium-bind
24	69.5	26.8	110	2	B48219 S-100 calcium-bind
25	68	26.3	90	1	BCHUY S-100 calcium-bind
26	68	26.3	98	2	JC5064 calcium-binding pr
27	68	26.3	98	2	JC5065 calcium-binding pr
28	67	25.9	90	1	S27011 calcyclin - rabbit
29	67	25.9	98	2	A41988 A-100 calcium-bind
30	65	25.1	217	2	J50330 26-kDa Ca2+-bindin

31	64	24.7	89	2	A54314 calcyclin - mouse
32	64	24.7	90	2	B28363 calcyclin - rat
33	63	24.3	102	1	J01300 calgizarin - rabb
34	61	23.6	97	2	A30129 S-100 protein, lun
35	61	23.6	469	2	S5167 IMF2-dependent sig
36	60.5	23.4	97	1	JH0663 calpactin I light
37	60.5	23.4	438	2	H72241 fixc protein - The
38	58.5	22.6	97	2	A28489 calpactin I light
39	57.5	22.2	2108	2	S28417 COC39 protein - ye
40	57	22.0	41	2	B42628 calcium-binding pr
41	56.5	21.8	95	1	L06G10 calpactin I light
42	56.5	21.8	97	2	JC1139 calpactin I light
43	56.5	21.8	97	2	B28489 calpactin I light
44	56.5	21.8	416	1	G64424 histidine--tRNA li
45	56	21.6	105	1	I37080 calgizarin - huma

ALIGNMENTS

RESULT 1
A55406
calgranulin c - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 23-May-1997
C:Accession: A55406
R:Del/Insert: A.C.; Schleicher, C.H.; Santome, J.A.
J. Biol. Chem. 269, 28929-28936, 1994
A:Title: Primary structure and binding properties of calgranulin C, a novel S100-like
A:Reference number: A55406; MUID:95050708
A:Accession: A55406
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-91
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; EF hand
F:48-80/Domain: calmodulin repeat homology <EF2>

Query Match 79.5% Score 206; DB 2; Length 91;
Best Local Similarity 82.0% Pred. No. 6e-19;
Matches 41; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Oy 1 TKLEDEHLEGIINIGHQYSVRGHPTLNKYEELKQLGTEKLPKTLQNXKQD 50
Db 1 TKLEDEHLEGIINIGHQYSVRGHPTLNKYEELKQLGTEKLPKTLQNXKQD 50
RESULT 2
JC4712
S-100 calcium-binding protein A12 - human
N:Alternate names: calcium-binding amniotic fluid protein 1 (CAAF1); calgranulin C; c
utrophin protein
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence_revision 19-Jun-1996 #text_change 13-Aug-1999
C:Accession: JC4712; JC4717; JC4891; S56113; S56114
R:Yamamura, T.; Hitomi, J.; Nagasaki, K.; Suzuki, M.; Takahashi, E.; Saito, S.; Tsuka
Biochem. Biophys. Res. Commun. 221, 356-360, 1996
A:Title: Human CAAF1 gene - molecular cloning, gene structure, and chromosome mapping
A:Reference number: JC4712; MUID:96192053
A:Accession: JC4712
A:Molecule type: mRNA
A:Residues: 1-92 <YAN>
A:Cross-references: DDBJ:D83657; NID:91502284; PIDN:BAAL2030.1; PID:91502285
R:Marli, T.; Ertmann, K.D.; Gallin, M.Y.
Biochem. Biophys. Res. Commun. 221, 454-458, 1996
A:Title: Host-parasite interaction in human onchocerciasis: Identification and sequen
A:Reference number: JC4717; MUID:96192069
A:Accession: JC4717
A:Molecule type: protein
A:Residues: 2-92 <MAR>
A:Experimental source: Onchocerca volvulus infecting human tissue
R:Ilg, E.C.; Troxler, H.; Buegesser, D.M.; Kuster, T.; Markert, M.; Guignard, F.; Hu

Blochem. Biophys. Res. Commun. 225, 146-150, 1996
 A.Title: Amino acid sequence determination of human S100 A12 (P6, Calgranulin C, CGRP, C
 A.Reference number: J04891; MUID:96332419
 A.Accession: J04891
 A.Molecule type: protein
 A.Residues: 2-92 <ILG>
 R:Guignard, F.; Manuel, J.; Markert, M.
 Blochem. J. 309, 395-401, 1995
 A.Title: Identification and characterization of a novel human neutrophil protein related
 A.Reference number: S56113; MUID:95351965
 A.Accession: S56113
 A.Status: preliminary
 A.Molecule type: protein
 A.Residues: 'xx',4-14,'X','16-17','xxxx' <GU11>
 A.Experimental source: Isoform 6a
 A.Accession: S56114
 A.Status: preliminary
 A.Molecule type: protein
 A.Residues: 2-21 <GUI2>
 A.Experimental source: Isoform 6b
 A.Comment: This protein is released by activated neutrophils in the course of inflammato
 nnelis:
 Gene: GDB:S100A12; p6; MRP6; CGRP; CAAP1
 A.Cross-references: GDB:5218374
 A.Map position: 1q21-1q21
 C:Complex: monomer
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: calcium binding; EF hand; monomer; neutrophil; zinc
 F:2-92/Product: S-100 calcium-binding protein A12 #status experimental <MAT>
 F:6-39/Domain: calmodulin repeat homology <EFI>
 F:49-81/Domain: calmodulin repeat homology <EFI>
 F:86-90/Region: zinc binding #status predicted

```

Query Match 73.0% Score 189; DB 2; Length 92;
Best Local Similarity 74.0%; Pred. No. 8e-17;
Matches 37; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 TLKLEHLEGIINIGHQSVYRGVHPTLNKYELEKQGTGTELPFTLONXKQ 50
|||||-----|||-----|||-----|||-----|||-----|||
DB 2 TLKEHLEGIIVNFHQSYSVRKHGFTLISKGELKQLTTEMLANTIKINMDK 51

RESULT 3

calgranulin B - bovine (fragment)
N:Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory factor
in 2
C:Species: Bos primigenius taurus (cattle)
Accession: B22309; Revision 23-May-1997 #text-change 23-May-1997
Date: 30-Sep-1993 #sequence
Submitting: T.K.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Chen,
submitted to the Protein Sequence Database, July 1992
A:Reference number: A22309
A:Accession: B22309
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-122 <TAN>
R:Dianoux, A.C.; Sasas, M.J.; Garin, J.; Gagnon, J.; Vignals, P.V.
Biochemistry 31, 5898-5905, 1992
A:Title: The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutrophils
A:Reference number: A42628; MUID:92304974
A:Accession: A42628
A:Molecule type: protein
A:Residues: 4-32, 'F', 34-56 <DIA>
C:Complex: heterodimer and higher complexes with calgranulin A
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; phospho
F:6-40/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>

Query Match 50.6% Score 131; DB 1; Length 122;

```

```

Best Local Similarity    56.2%, Pred. No. 1,9e+09;
Matches   27; Conservative   8; Mismatches  13; Indels      0; Gaps      0;

OY      1 TKLEHLEGITNIGHQIVRVGHEDTLNKLYKLGKLPKLTQNKK 48
       :::: : |||| ||||||:::||| : ||| |||| : 
Db      2 SOMESSIEIINIFHOYSVRGLGHTLIQKESKOLVOKELPNFKK 49

RESULT  4
JN0686

calgranulin B -rat
N:Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory fa
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-May-1994 #sequence revision 23-May-1997 #text_change 22-Jun-1999
C:Accession: JN0686
R:Imimichl, T.; Uchida, I.; Wahl, S.M.; McCartney-Francis, N.
Biochem. Biophys. Res. Commun. 194, 819-825, 1993
A:Title: Expression and cloning of migration inhibitory factor-related protein (MRP)8
A:Reference number: JN0685; MUID:93343942
A:Accession: JN0686
A:Molecule type: mRNA
A:Residues: 1-113 <IMA>
A:Cross-references: GB:U18948; NID:g488156; PIDN:AAA1214.1; PID:g488157
C:Genetics:
A:Gene: MRP14
C:Complex: heterodimer and higher complexes with calgranulin A
C:Keywords: S-100 protein; calmodulin repeat homology
C:Keywords: acetylated amino end; calcium binding; EF hand; heterodimer; inflammation
F:1-113/Product: calgranulin B #status predicted <MAT>
F:1-45/Domain: calmodulin repeat homology <EF1>
F:55-87/Domain: calmodulin repeat homology <EPF>
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F:80-91/Disulfide bonds: #status predicted

```

```

Query Match      44.0% Score 114; DB 1; Length 113;
Best Local Similarity 47.9%; Pred. No. 2,3e-07;
Matches 23; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

OY      1 TKLEDHLEGIINIGHQYSVVRGVHEDTLNKKYEKLKGLPEPTLQNKK 48
          ::::: |||: ||||: | | ||||: |::: ||: ||: |
DB       7 SOLERSISTIIIVFHQYSRKYGHPDTLNKAFFKEEMWNKDLPNFLKRK 54

RESULT   5

B31848
calgranulin B - human
N.Alternate names: calcium-binding protein MRP-14; cystic fibrosis-associated antigen
(MRP-14); MIF-related 14k protein; S-100 calcium-binding protein A9 (S100A9)
C.Species: Homo sapiens (man)
C.Date: 21-May-1990 #sequence_revision 23-May-1997 #text_change 22-Jun-1999
C.Accession: B31848; S00667; A33819; B60911; B61082; D54527
R.Lagasse, E.; Clerc, R.G.
Mol. Cell. Biol. 8, 2402-2410, 1988
A.Title: Cloning and expression of two human genes encoding calcium-binding proteins
A.Reference number: A93102; MUID:88302148
A.Accession: B31848
A.Molecule type: DNA
A.Residues: 1-114 <LAG>
A.Cross-references: GB:421064; NID:g188689; PIDN:AAA36326.1; PID:g386958
R.Oldink, K.; Cerletti, N.; Brueggen, J.; Clerc, R.G.; Tarcsey, L.; Zwadlo, G.; Gerhar
Nature 330, 80-82, 1987
A.Title: Two calcium-binding proteins in infiltrate macrophages of rheumatoid arthritis
A.Reference number: S00667; MUID:88039099
A.Accession: S00667
A.Molecule type: mRNA
A.Residues: 1-114 <OMI>
A.Cross-references: EMBL:X06233; NID:g34770; PIDN:CAA29579.1; PID:g34771
A.Note: Parts of this sequence were confirmed by protein sequencing
R.Murao, S.; Collart, F.R.; Huberman, E.
J. Biol. Chem. 264, 8356-8360, 1989
A.Title: A protein containing the cystic fibrosis antigen is an inhibitor of protein
A.Reference number: A33819; MUID:89255276

```

A:Accession: A33819
 A:Molecule type: mRNA
 A:Residues: 1-114 <MUR>
 A:Cross-references: GB:M26311; NID:g862619; PID:g516621
 A>Note: part of this sequence was confirmed by protein sequencing; the amino end of the R:Andersson, K.B.; Sletten, K.; Bernitz, H.B.; Dale, I.; Erandzaag, P.; Jellum, E.; Fa Scand. J. Immunol. 28, 241-245, 1988
 A:Title: The leucocyte L1 protein: identity with the cystic fibrosis antigen and the cal A:Reference number: A60911; MUID:88321575
 A:Accession: B60911
 A:Molecule type: protein
 A:Residues: 39-42, 'X', 44-50, 64-77, 'X', 79, 84, 'X', 86-90, 'X', 92-94, 'X', 96-98 <AND>
 R:Tobe, T.; Murakami, K.; Tomita, M.; Nozawa, R.
 Chem. Pharm. Bull. 37, 1576-1580, 1989
 A:Title: Amino acid sequences of 60B8 antigens induced in HL-60 cells by 1,25-dihydroxy A:Reference number: A61082; MUID:89376638
 A:Accession: B61082
 A:Molecule type: protein
 A:Residues: 5-77, 80-90, 'A', 92-114 <TOB>
 A:Note: the blocked amino end of the mature protein is identified as 2-Thr; residue 91-H Rasmussen, P.; Rasmussen, H.H.; Jeffers, H.; Honore, B.; Dejgaard, K.; Olsen, E.; Kill, J E.
 J. Invest. Dermatol. 97, 701-712, 1991
 A:Title: Molecular cloning, occurrence, and expression of a novel partially secreted pro A:Reference number: A54327; MUID:92043866
 A:Accession: D54327
 A:Molecule type: protein
 A:Residues: 11-19, 26-38, 94-105, 'X', 107 <MAD>
 A:Note: In several peptide samples no PTH was detected for 95-His but in one peptide PTH C:Comment: This protein appears to be expressed only in cells of myeloid origin actively C:Genetics: The presence of 3'-methylhistidine at position 105, corresponding to 107-His C:Gene: GDB:SI0069; 608BAG; CAGB; CFAG; LIAG; MAC387; MIF; MRP14; NIF; P14
 A:Cross-references: GDB:120570; OMIM:123886
 A:Map position: 1q21-1q21
 A:Introns: 50/3
 A:Note: the first intron occurs before the initiator codon
 C:Complex: heterodimer and higher complexes with calgranulin A (see PIR:BCNUCF)
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; phos F:2-114/Product: calgranulin B #status experimental <MAY>
 F:10-44/Domain: calmodulin repeat homology <EF1>
 F:54-86/Domain: calmodulin repeat homology <EF2>
 F:2/Modified site: blocked amino end (Thr) (in mature form) (probably acetylated) #statu F:113/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 42.5%; Score 110; DB 1; Length 114;
 Best local similarity 51.1%; Pred. No. 7.4e-07;
 Matches 23; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

DB 6 S0LERNIETITTFHQYSVKLGHPDTLNQGFELVRDQNFLEK 50

RESULT 6
 S06207
 calvasculin - mouse
 N:Alternate names: calcium-binding protein mts1; calcium-binding protein PEL88; placenta C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text change 13-Aug-1999
 C:Accession: S06207; JH0097; A26803; A41411; I48674
 R:Ebratidze, A.; Tulchinsky, E.; Grigorian, M.; Afanasyeva, A.; Senin, V.; Revazova, E.; Genes Dev. 3, 1086-1093, 1989
 A:Title: Isolation and characterization of a gene specifically expressed in different me A:Reference number: S06207; MUID:89378739
 A:Accession: S06207
 A:Molecule type: mRNA
 A:Residues: 1-101 <EBR>
 A:Cross-references: EMBL:X16190; NID:g54926; PIDN:CAA34316.1; PID:g54927
 R:Tulchinsky, E.M.; Grigorian, M.S.; Ebratidze, A.K.; Mishina, N.I.; Lukanidin, E.M.

Gene 87, 219-223, 1990
 A:Title: Structure of gene mts1, transcribed in metastatic mouse tumor cells.
 A:Reference number: JH0097; MUID:90236313
 A:Accession: JH0097
 A:Molecule type: DNA
 A:Residues: 1-101 <TUL>
 A:Cross-references: GB:M36578; GB:M36579
 A:Experimental source: liver
 R:Tulchinsky, B.
 Submitted to the EMBL Data Library, August 1989
 A:Reference number: S07981
 A:Accession: S07981
 A:Molecule type: DNA
 A:Residues: 1-47, 'VSGSXENG', 56-57, 'RTDEA' <TU2>
 A:Cross-references: EMBL:X16094; NID:g53249; PIDN:CAA34224.1; PID:g53250
 R:Jackson-Crumbly, L.L.; Swerfel, J.; Linzer, D.I.H.
 Nucleic Acids Res. 15, 6677-6690, 1987
 A:Title: A growth-related mRNA in cultured mouse cells encodes a placental calcium bi A:Reference number: A26803; MUID:87316927
 A:Accession: A26803
 A:Molecule type: preliminary
 A:Status: preliminary
 A:Residues: 1-101 <JAC>
 A:Cross-references: GB:X05835; NID:g50310; PIDN:CAA29282.1; PID:g50311
 R:Goto, K.; Endo, H.; Fujiyoshi, T.
 J. Biochem. 103, 48-53, 1988
 A:Title: Cloning of the sequences expressed abundantly in established cell lines: ide A:Reference number: A41411; MUID:8818109
 A:Accession: A41411
 A:Status: preliminary
 A:Molecule type: preliminary
 A:Residues: 1-101 <GCT>
 A:Cross-references: GB:D00208; NID:g220569; PIDN:BA00148.1; PID:di000593; PID:g22057 R:Tulchinsky, E.; Kramarov, D.; Ford, H.L.; Reshetnyak, E.; Lukanidin, E.; Zain, S.
 Oncogene 8, 79-86, 1993
 A:Title: Characterization of a positive regulatory element in the mts1 gene.
 A:Reference number: I48674; MUID:93141279
 A:Accession: I48674
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-47, 'VSGSXENG', 48-54 <RES>
 A:Cross-references: EMBL:X16094; NID:g53249; PIDN:CAA34224.1; PID:g53250
 C:Comment: Gene mts1 is expressed in metastatic cells.
 C:Genetics:
 A:Gene: mts1
 A:Introns: 47/3
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: calcium binding; cancer; EF hand
 F:7-41/Domain: calmodulin repeat homology <EF1>
 F:50-82/Domain: calmodulin repeat homology <EF2>

Query Match 34.4%; Score 89; DB 2; Length 101;
 Best local similarity 43.8%; Pred. No. 0.00027;
 Matches 21; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

DB 5 LEELDVIVSTFKYSGKDGKFKLTKELTLRELPSFLGRTRDE 52

RESULT 7
 S24146
 S-100 protein P - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text change 13-Aug-1999
 C:Accession: S24146; P50340
 R:Becker, T.; Gerke, V.; Kube, E.; Weber, K.
 Eur. J. Biochem. 207, 541-547, 1992
 A:Title: S100P, a novel Ca(2+)-binding protein from human placenta. cDNA cloning, rec A:Reference number: S24146; MUID:92339442
 A:Accession: S24146
 A:Status: preliminary

Tue Mar 14 17:41:52 2000

us-09-167-705-2.rpt

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 14, 2000, 15:45:10 ; Search time 8.39 Seconds
(without alignments)
177,979 Million cell updates/sec

Title: US-09-167-705-2

Perfect score: 259
Sequence: 1 TKLEDHLEGINIGHQSVR.....ELKQVGTKEIKPTLQNXKQD 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	88.8	91	1	S112_BOVIN
2	206	79.5	91	1	S112_PYG
3	189	73.0	91	1	S112_HUMAN
4	136	52.5	81	1	S112_RABIT
5	133	51.4	122	1	S109_BOVIN
6	114	44.0	113	1	S109_RAT
7	110	42.5	114	1	S109_HUMAN
8	94	36.3	118	1	S109_RABIT
9	94	36.3	119	1	M126_CHICK
10	89	34.4	101	1	S104_MOUSE
11	87	33.6	95	1	S108_HUMAN
12	87	33.6	101	1	S104_RAT
13	84	32.4	91	1	S108_HUMAN
14	84	32.4	91	1	S108_MOUSE
15	84	32.4	91	1	S108_RAT
16	83	32.0	91	1	S108_BOVIN
17	83	32.0	100	1	S104_BOVIN
18	83	32.0	101	1	S104_HUMAN
19	78	30.1	112	1	S108_MOUSE
20	74	28.6	93	1	S108_HUMAN
21	73	28.2	88	1	S108_MOUSE
22	72	27.8	92	1	S101_ICTPU
23	71	27.4	93	1	S106_HORSE
24	71	27.4	93	1	S108_BOVIN
25	71	27.4	93	1	S108_HUMAN
26	70	27.0	88	1	S108_RAT
27	70	27.0	93	1	S108_RAT
28	69.5	26.8	110	1	S105_HUMAN
29	68	26.3	90	1	S106_HUMAN
30	68	26.3	93	1	S10A_MOUSE
31	68	26.3	98	1	S113_HUMAN
32	68	26.3	98	1	S113_MOUSE
33	67	25.9	90	1	S106_RABIT
34	67	25.9	97	1	S102_HUMAN

35	64	24.7	89	1	S106_MOUSE	P14069 mus musculus
36	64	24.7	90	1	S106_RAT	P05964 rattus norv
37	64	24.7	93	1	S105_MOUSE	O08945 mus musculus
38	63	24.3	102	1	S111_RABIT	P24480 oryctolagus
39	61	23.6	97	1	S102_BOVIN	P10462 bos taurus
40	61	23.6	469	1	ID82_YEAST	P46958 saccharomyc
41	60.5	23.4	96	1	S110_CHICK	P27003 gallus gall
42	60	23.2	92	1	S106_CHICK	O08953 gallus gall
43	59.5	23.0	101	1	S107_BOVIN	O28050 bos taurus
44	58.5	22.6	96	1	S110_MOUSE	P08207 mus musculus
45	57.5	22.2	2108	1	NOT1_YEAST	P25655 saccharomyc

ALIGNMENTS

RESULT 1	S112_BOVIN	STANDARD;	PRT;	91 AA.
AC	P79105;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	CALGRANDIN C (CAGC) (CALCIUM-BINDING PROTEIN IN AMNIOTIC FLUID 1) (CAAF1).			
GN	S100A12 OR CAAF1.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;			
OC	Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;			
OC	Bovinae; Bos.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-OESOPHAGUS;			
RX	MEDLINE; 96298783.			
RA	HITOMI J., YAMAGUCHI K., KIKUCHI Y., KIMURA T., MARYAMA K.,			
RA	NAGASAKI K.;			
RT	"A novel calcium-binding protein in amniotic fluid, CAAF1: its			
RT	molecular cloning and tissue distribution.";			
RL	J Cell Sci. 109:805-815(1996)			
CC	1. SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND			
CC	MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; DA9548; BA08496.1; -			
DR	HSSP; P02633; IBOC.			
DR	PROSITE; PS00018; EF_HAND.1.			
DR	PROSITE; PS00303; S100_CABP.1.			
DR	PFAM; PF00036; efhand.1.			
DR	PFAM; PF01023; S100.1.			
KW	Calcium-binding; zinc; Metal-binding.			
FT	INIT-MET 0			
FT	CA-BIND 18 31			
FT	CA-BIND 61 72			
FT	SEQUENCE 91 AA; 10554 MW; AC40069C CRC32;			

Query Match 88.8%; Score 230; DB 1; Length 91;
Best local Similarity 92.0%; Pred. No. 6,9e-23;
Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY	1 TKLEDHLEGINIGHQSVRGFDLTKYELKQVGTKEIKPTLQNXKQD 50
DB	1 TKLEDHLEGINIGHQSVRGFDLTKYELKQVGTKEIKPTLQNXKQD 50
RESULT	2

S112_PIG STANDARD; PRT; 91 AA.
 ID S112_PIG
 AC P80310;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CALGRANULIN C (CAGC).
 GN S100A12.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-GRANULOCYTE;
 RX MEDLINE; 95050708.
 RA DELL'ANGELO E.C., SCHLEICHER C.H., SANTOME J.A.;
 RT "Primary structure and binding properties of calgranulin C, a novel
 RT S100-like calcium-binding protein from pig granulocytes.";
 RL J. Biol. Chem. 269:28929-28936(1994)
 CC -1- TISSUE SPECIFICITY: FOUND ESSENTIALLY IN GRANULOCYTES WITH SMALL
 CC AMOUNTS FOUND IN LYMPHOCYTES.
 CC -1- MISCELLANEOUS: IN THE ABSENCE OF ZINC BINDS ONE CALCIUM ION PER
 CC MOLECULE. IN THE PRESENCE OF ZINC BINDS TWO CALCIUM IONS PER
 CC MOLECULE.
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
 CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
 DR HSSP; P02632; ICB1.
 DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
 DR PROSITE; PS00303; S100_CABP; 1.
 DR PFAM; PF00036; efhand; 1.
 DR PFAM; PF01023; S_100; 1.
 KM Calcium-binding; zinc; Metal-binding.
 FT CA_BIND 18 31 SITE I (LOW AFFINITY) (BY SIMILARITY).
 FT CA_BIND 61 72 SITE II (HIGH AFFINITY) (BY SIMILARITY).
 SQ SEQUENCE 91 AA; 10614 MW; D2B5F6EF CRC32;
 OY 1 TKLEHLEGIINIGHOYSVRGHFDLTKYELKQLGTKEPLTKLONKKDQ 50
 DB 1 TKLEHLEGIINIGHOYSVRGHFDLTKYELKQLGTKEPLTKLONKKDQ 50
 RESULT 3
 S112_HUMAN STANDARD; PRT; 91 AA.
 ID S112_HUMAN
 AC P80511;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CALGRANULIN C (CAGC) (P6) (CGRP) (NEUTROPHIL S100 PROTEIN) (CALCIUM-
 DE BINDING PROTEIN IN AMNIOTIC FLUID 1) (CAAF1).
 GN S100A12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97138564.
 RA WICKI R., NARENHOLZ I., MISCHKE D., SCHAEFER B.W., HEIZMANN C.W.;
 RT "Characterization of the human S100A12 (calgranulin C, p6, CAAF1,
 RT CGRP) gene, a new member of the S100 gene cluster on chromosome
 RT 1921.";
 RL Cell Calcium 20:459-464(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96192053.
 RA YAMAMURA T., HITOMI J., NAGASAKI K., SUZUKI M., TAKAHASHI E.,
 RA SAITO S., TSUKADA T., YAMAGUCHI K.;
 RT "Human CAAF1 gene -- molecular cloning, gene structure, and chromosome

RT mapping.";
 RL Biochem. Biophys. Res. Commun. 221:356-360(1996).
 RN [3]
 RP SEQUENCE.
 RX MEDLINE; 96192069.
 RA MARTI T., ERTTMANN K.D., GALLIN M.Y.;
 RT "Host-parasite interaction in human onchocerciasis: Identification
 RT and sequence analysis of a novel human calgranulin.";
 RL Biochem. Biophys. Res. Commun. 221:454-458(1996).
 RN [4]
 RP SEQUENCE.
 RC TISSUE-NEUTROPHILS;
 RX MEDLINE; 96332419.
 RA IIG E.C., TROXLER H., BUEGESSER D.M., KOSTER T., MARKERT M.,
 RA GUIGNARD F., HUNZIKER P., BIRCHLER N., HEIZMANN C.W.;
 RT "Amino acid sequence determination of human S100A12 (p6, calgranulin
 RT C, CGRP, CAAF1) by tandem mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 225:146-150(1996).
 RN [5]
 RP SEQUENCE OF 1-20.
 RX MEDLINE; 95351965.
 RA GUIGNARD F., MAUEL J., MARKERT M.;
 RT "Identification and characterization of a novel human neutrophil
 RT protein related to the S100 family.";
 RL Biochem. J. 309:395-401(1995).
 CC -1- SUBUNIT: MONOMER.
 CC -1- TISSUE SPECIFICITY: MONOCYTES AND LYMPHOCYTES.
 CC -1- MASS SPECTROMETRY: MW=10444; METHOD=ELECTROSPRAY.
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
 CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
 CC -----
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 DR EMBL; X98580; CAA66934.1; JOINED.
 DR EMBL; X98581; CAA66934.1; JOINED.
 DR EMBL; X98582; CAA66934.1; JOINED.
 DR EMBL; X98583; CAA66934.1; JOINED.
 DR EMBL; X98584; CAA66934.1; JOINED.
 DR EMBL; X98585; CAA66934.1; JOINED.
 DR EMBL; X98586; CAA66934.1; JOINED.
 DR EMBL; X98587; CAA66934.1; JOINED.
 DR EMBL; X98588; CAA66934.1; JOINED.
 DR EMBL; X98589; CAA66934.1; JOINED.
 DR EMBL; X98590; CAA66934.1; JOINED.
 DR EMBL; X98591; CAA66934.1; JOINED.
 DR EMBL; X98592; CAA66934.1; JOINED.
 DR EMBL; X98593; CAA66934.1; JOINED.
 DR EMBL; X98594; CAA66934.1; JOINED.
 DR EMBL; X98595; CAA66934.1; JOINED.
 DR EMBL; X98596; CAA66934.1; JOINED.
 DR EMBL; X98597; CAA66934.1; JOINED.
 DR EMBL; X98598; CAA66934.1; JOINED.
 DR EMBL; X98599; CAA66934.1; JOINED.
 DR EMBL; X98600; CAA66934.1; JOINED.
 DR EMBL; X98601; CAA66934.1; JOINED.
 DR EMBL; X98602; CAA66934.1; JOINED.
 DR EMBL; X98603; CAA66934.1; JOINED.
 DR EMBL; X98604; CAA66934.1; JOINED.
 DR EMBL; X98605; CAA66934.1; JOINED.
 DR EMBL; X98606; CAA66934.1; JOINED.
 DR EMBL; X98607; CAA66934.1; JOINED.
 DR EMBL; X98608; CAA66934.1; JOINED.
 DR EMBL; X98609; CAA66934.1; JOINED.
 DR EMBL; X98610; CAA66934.1; JOINED.
 DR EMBL; X98611; CAA66934.1; JOINED.
 DR EMBL; X98612; CAA66934.1; JOINED.
 DR EMBL; X98613; CAA66934.1; JOINED.
 DR EMBL; X98614; CAA66934.1; JOINED.
 DR EMBL; X98615; CAA66934.1; JOINED.
 DR EMBL; X98616; CAA66934.1; JOINED.
 DR EMBL; X98617; CAA66934.1; JOINED.
 DR EMBL; X98618; CAA66934.1; JOINED.
 DR EMBL; X98619; CAA66934.1; JOINED.
 DR EMBL; X98620; CAA66934.1; JOINED.
 DR EMBL; X98621; CAA66934.1; JOINED.
 DR EMBL; X98622; CAA66934.1; JOINED.
 DR EMBL; X98623; CAA66934.1; JOINED.
 DR EMBL; X98624; CAA66934.1; JOINED.
 DR EMBL; X98625; CAA66934.1; JOINED.
 DR EMBL; X98626; CAA66934.1; JOINED.
 DR EMBL; X98627; CAA66934.1; JOINED.
 DR EMBL; X98628; CAA66934.1; JOINED.
 DR EMBL; X98629; CAA66934.1; JOINED.
 DR EMBL; X98630; CAA66934.1; JOINED.
 DR EMBL; X98631; CAA66934.1; JOINED.
 DR EMBL; X98632; CAA6693

DT 15-JUL-1999 (Rel. 38, last sequence update)
 DT 15-JUL-1999 (Rel. 38, last annotation update)
 DE CALGRANDLIN C (CAGC) (FRAGMENT).
 GN S100A12.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=NEW ZEALAND WHITE; TISSUE=NEUTROPHILS;
 RX MEDLINE; 96355278.
 RA YANG Z., DEVEYER M.J., GARDINER E.E., DEVENISH R.J., HANDLEY C.J.,
 RA UNDERWOOD J.R., ROBINSON H.C.;
 RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
 calgranulin C when incubated with inorganic [35S]sulfate."
 RL J. Biol. Chem. 271:19802-19809(1996).
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
 CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
 CC -----
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 CC -----
 DR EMBL: AF091848; AAC61770.1; -
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00303; S100_CABP; 1.
 DR PFAM; PF00036; efhand; 1.
 DR PFAM; PF01023; S_100; 1.
 KM Calcium-binding.
 FT NON_TER 1 1 SITE I (LOW AFFINITY) (BY SIMILARITY).
 FT CA_BIND 8 21 SITE II (HIGH AFFINITY) (BY SIMILARITY).
 FT CA_BIND 51 62 SITE II (HIGH AFFINITY) (BY SIMILARITY).
 SO SEQUENCE 81 AA; 9401 MW; 4AE11912 CRC32;

 Query Match 52.5%; Score 136; DB 1; Length 81;
 Best Local Similarity 67.5%; Pred. No. 6.7e-11;
 Matches 27; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

 QY 11 INIGHQYSVRGHFDLTKYELKQKELPKTLQNXK 50
 ||| ||||| ||:||||: |||: ||| ||| |||
 Db 1 INFHQYSVRGHFDLTKYELKQKELPKTLQNXK 40

 QY 5
 S109_BOVIN STANDARD; PRT; 122 AA.
 AC P28783;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-JUL-1993 (Rel. 26, last sequence update)
 DT 01-OCT-1996 (Rel. 34, last annotation update)
 DE CALGRANDLIN B (NEUTROPHIL CYTOSOLIC 23 KD PROTEIN) (P23) (BEE22)
 DE (FRAGMENT).
 GN S100A9.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae;
 OC Bovinae; Bos.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=ESOPHAGEAL EPITHELIUM;
 RX MEDLINE; 93280230.
 RA TANG T.R., HONG T.-M., LIN C.-Y., LAI M.-L., LIU C.H.L., LO H.-J.,
 RA WANG M.-E., CHEN L.B., CHEN W.-T., IP W., LIN D.C., LIN J.J.-C.,
 RA LIN S., SUN T.-T., WANG E., WANG J.L., WU R., WU C.-W., CHEN S.;
 RT "Nuclear proteins of the bovine esophageal epithelium. I. Monoclonal
 RT antibody W2 specifically reacts with condensed nuclei of
 RT differentiated superficial cells."
 RT J. Cell Sci. 104:237-247(1993).

RN [2]
 RP SEQUENCE OF 4-56.
 RC TISSUE=NEUTROPHILS;
 RX MEDLINE; 92304974.
 RA DIANOUX A.-C., STASIA M.-J., GARIN J., GAGNON J., VIGNAIS P.V.;
 RT "The 23-kilodalton protein, a substrate of protein kinase C, in
 RT bovine neutrophil cytosol is a member of the S100 family."
 RL Biochemistry 31:5898-5905(1992).
 CC -1- SUBUNIT: DISULFIDE LINKED HETERODIMER OF A 7/11 KD AND A 22/23 KD
 CC SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC; LOOSELY ASSOCIATED TO THE
 CC CYTOSKELETON.
 CC -1- TISSUE SPECIFICITY: FOUND ESSENTIALLY IN PHAGOCYTTIC CELLS.
 CC -1- PTM: PHOSPHORYLATED BY PROTEIN KINASE C.
 CC -1- MISCELLANEOUS: CONTAINS TWO CA(2+)-BINDING DOMAINS PER PROTEIN.
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
 CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
 DR HSSP; P02638; ICFP.
 DR PROSITE; PS00018; EF_HAND; PARTIAL.
 DR PROSITE; PS00303; S100_CABP; 1.
 DR PFAM; PF00036; efhand; 1.
 DR PFAM; PF01023; S_100; 1.
 KM Calcium-binding; Phosphorylation.
 FT NON_TER 1 1
 FT CA_BIND 19 32 SITE I (LOW AFFINITY) (POTENTIAL).
 FT CA_BIND 53 64 SITE II (HIGH AFFINITY) (POTENTIAL).
 SO SEQUENCE 122 AA; 13673 MW; 7A313AFD CRC32;

 Query Match 51.4%; Score 133; DB 1; Length 122;
 Best Local Similarity 56.2%; Pred. No. 2.6e-10;
 Matches 27; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

 QY 1 TKLEDEHGIINIGHQYSVRGHFDLTKYELKQKELPKTLQNXK 48
 ::||: ||||| |||||: |||||: ||| ||||| |||
 Db 2 SQHSEIETIINIFHQYSVRGHFDLTKYELKQKELPKTLQNXK 49

 RESULT 6
 S109_RAT STANDARD; PRT; 113 AA.
 ID S109_RAT
 AC P50116;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 01-OCT-1996 (Rel. 34, last annotation update)
 DE CALGRANDLIN B (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 14)
 DE (MRP-14).
 GN S100A9 OR MRP14.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LEWIS/N; TISSUE=PERITONEAL CAVITY;
 RX MEDLINE; 93343942.
 RA IWAMICHI T., UCHIDA I., WAHL S.M., MCCARTNEY-FRANCIS N.;
 RT "Expression and cloning of migration inhibitory factor-related
 RT protein (MRP) 8 and MRP14 in arthritis-susceptible rats."
 RL Biochem. Biophys. Res. Commun. 194:819-825(1993).
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
 CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
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 CC -----
 DR EMBL: L18948; AAA18214.1; -
 DR HSSP; P04271; IUWO.
 DR PROSITE; PS00018; EF_HAND; FALSE_NEG.


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FA MOREI S., GOTO K., GOTO F., MUTAKAMI K., OKAMAWA S., YOSHINAGA M.;
RT "Dynamic changes in mRNA expression of neutrophils during the course
RT of acute inflammation in rabbits.";
RL Int. Immunol. 6:149-156(1994).
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
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CC -----
CC DR EMBL; AF091849; AAC61771.1; -.
CC DR EMBL; D17404; BAA04227.1; -.
CC DR PROSITE; PS00018; EF_HAND; 1.
CC PROSITE; PS00303; S100_CABP; 1.
CC PFM; PF00036; ehand; 1.
CC Calcium-binding; Repeat.
CC FT NON_TER 1 1
CC FT CA_BIND 9 22 SITE I (LOW AFFINITY) (POTENTIAL).
CC FT CA_BIND 64 64 SITE II (HIGH AFFINITY) (POTENTIAL).
CC FT DOMAIN 103 118 2 x 8 AA TANDEN REPEATS OF G-H-G-H-
CC FT REPEAT 103 110 1.
CC FT REPEAT 111 118 2.
CC SO SEQUENCE 118 AA; 13292 MW; 0D7899DD CRC32;
CC -----
Oy Query Match 36.3%; Score 94; DB 1; Length 118;
Best Local Similarity 61.1%; Pred. No. 2.5e-05;
Matches 22; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
Db 1 IINIGHQSVRYGHEDTLNKYELQGTREKPKTKQ 45
||||| ||||| |||:| ||| |||
1 IINIFHQTSVRYGPPDLSQKEFKQVQKEHNFUK 36
-----
RESULT 9
ID M126_CHICK STANDARD; PRT; 119 AA.
AC P28318;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
PRTIN MRP-126
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
[1]
SEQUENCE FROM N.A.
RP STRAIN-WHITE LEGHORN; TISSUE-BONE MARROW;
RC MEDLINE; 92195690.
RX MAKANO T., GRAF T.;
RA "Identification of genes differentially expressed in two types of
RT v-myb-transformed avian myelomonocytic cells.";
RL Oncogene 7:527-534(1992).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN V-MYB-TRANSFORMED MYELOMONOCYTIC
CC CELLS.
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
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CC -----
CC DR EMBL; X61200-; NOT_ANNOTATED_CDS.

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DR HSSP: P04271; IUWO.
DR PROSITE: PS00018; EF HAND; 1.
DR PROSITE: PS00303; S100_CABP; 1.
DR PFAM: PF00036; ethand; 1.
DR PFAM: PF01023; S_100; 1.
KW Calcium-binding.
FT CA BIND 29 42 SITE I (LOW AFFINITY) (POTENTIAL).
FT CA BIND 72 83 SITE II (HIGH AFFINITY) (POTENTIAL).
SQ SEQUENCE 119 AA: 14065 MW; 25718D2B CRC32;

Query Match      36.3%; Score 94; DB 1; Length 119;
Best Local Similarity 44.0%; Pred No. 2.5e-05;
Matches 22; Conservative 11; Mismatches 17; Indels 0; Gaps 0

Db      12 SELECTAIDVIDVHFQYSRREDKDTLRRLKRLKLLEKQLANLYLKHVKNG 61
       1 TKLEDLEGIIIGHQYSVRGHFDTLKKELKQLGTRELPKTLQNKKDD 50
       :|::||::||::||::||::||::||::||::||::||::||::||::||:
       12 SELEKAIDVIDVHFQYSRREDKDTLRRLKRLKLLEKQLANLYLKHVKNG 61

RESULT 10
S104_MOUSE STANDARD: PTR; 101 AA.
ID S104_MOUSE STANDARD: PTR; 101 AA.
AC P07091; P20066;
DT 01-APR-1988 (rel. 07, Created)
DT 01-APR-1988 (rel. 07, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE PLACENTAL CALCIUM-BINDING PROTEIN (18A2) (PEP98) (MTS1 PROTEIN)
DE (METASTATIC CELL PROTEIN).
GN S100M4 OR CAPL OR MTS1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE: 87316927.
RA JACKSON-GROSS R.L.B., SWIERGIEL J., LINZER D.I.H.;
RT "A growth-related mRNA in cultured mouse cells encodes a placental
RT calcium binding protein."
RL Nucleic Acids Res. 15:6677-6690(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE: 88198109.
RA GOTO K., ENDO H., FUJIOCHI T.;
RT "Cloning of the sequences expressed abundantly in established cell
RT lines: identification of a cDNA clone highly homologous to S-100, a
RT calcium binding protein."
RL J. Biochem. 103:48-53(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE: 89376739.
RX ERRATIDE A., TUCHINSKY E., GRIGORIAN M., APANASYEVA A., SEMIN V.,
RA REVAKOVA E., LUKANIDIN E.;
RT "Isolation and characterization of a gene specifically expressed in
RT different metastatic cells and whose deduced gene product has a high
RT degree of homology to a Ca2+-binding protein family."
RL Genes Dev. 3:1086-1093(1989).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE: 9023613.
RA TUCHINSKY E.M., GRIGORIAN M.S., ERBALDZE A.K., MILSHINA N.I.,
RA LUKANIDIN E.M.;
RT "Structure of gene mts1, transcribed in metastatic mouse tumor
RT cells."
RL Gene 87:219-223(1990).
RN [5]
RP SEQUENCE OF 1-54 FROM N.A.
RX MEDLINE: 93141279.
RA TUCHINSKY E., KRAMEV D., FORD H.L., RESHETNYAK E., LUKANIDIN E.,
RA ZAIN S.;
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RT      "Characterization of a positive regulatory element in the mtsl gene.";
RL      Oncogene 8:79-86(1993) .
CC      -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DIFFERENT METASTATIC
CC      CELLS.
CC      -1- INDUCTION: THE MRNA CODING FOR THIS PROTEIN INCREASES IN
CC      ABUNDANCE AFTER SERUM STIMULATION OF QUIESCENT MOUSE FIBROBLASTS.
CC      -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
CC      MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
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CC      -----
DR      DR      EMBL; X05835; CAA29282.1; -
DR      DR      EMBL; D00028; BAA00148.1; -
DR      DR      EMBL; M36578; AAA39749.1; -
DR      DR      EMBL; M36579; AAA39750.1; -
DR      DR      EMBL; X16190; CAA34316.1; -
DR      DR      EMBL; X16094; CAA34224.1; -
DR      DR      PIR; A26803; A26803.
DR      DR      PIR; S06207; S06207.
DR      DR      PIR; A41411; A41411.
DR      DR      HSSP; P30801; ICNP.
DR      DR      MGJ; MGI:1330282; S100A4.
DR      DR      PROSITE; PS00018; EF_HAND; 1.
DR      DR      PROSITE; PS00303; S100_CABP; 1.
DR      DR      PFAM; PF00036; efhand; 1.
DR      DR      PFAM; PF01023; S_100; 1.
KW      Calcium-binding; Placenta.
FT      CA_BIND 20 33 SITE I (LOW AFFINITY) (POTENTIAL).
FT      CA_BIND 63 74 SITE II (HIGH AFFINITY) (POTENTIAL).
FT      CONFLICT 47 47 G->GVSQSPNGO (IN REF. 5).
SQ      SEQUENCE 101 AA; 11721 MM; AD26346E CRC32;

Query Match          34.4%; Score 89; DB 1; Length 101;
Best Local Similarity 43.8%; Pred. No. 9.1e-05;
Matches 21; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY      3 LEDHEGLIINIGHQSVRGHFDTLNKYLEKQLGTRELPKTQNKKQD 50
DY      11 : : : : : : : : : : : : : : : : : : : : : : : :
DB      5 LEEDADVIVSTFHKYSGRKGDKFKLNKLTRELPSFLGKRTRDE 52

RESULT 11
#E_HUMAN
AC      S100_HUMAN STANDARD: PRT; 95 AA.
MC      P25815;
DT      01-MAY-1992 (Rel. 22, Created)
DT      01-DEC-1992 (Rel. 24, Last sequence update)
DT      01-FEB-1996 (Rel. 33, Last annotation update)
DE      S-100P PROTEIN.
GN      S100P OR S100P.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      TISSUE=PLACENTA;
RX      MEDLINE; 92339442.
RA      BECKER T., GERKE V., KUBE E., WEBER K.;
RT      "S100P, a novel Ca(2+)-binding protein from human placenta. cDNA
RT      cloning, recombinant protein expression and Ca2+ binding
RT      properties.";
RL      Eur. J. Biochem. 207:541-547(1992).
RP      [2]
RP      SEQUENCE OF 1-91.
RX      TISSUE=PLACENTA;
RX      MEDLINE; 92171935.
```

RA	EMOTO Y KOBAYASHI R., AKATSUKA H., HIDAKA H.:
RT	"Purification and characterization of a new member of the S-100
RL	protein family from human Placenta."
RH	Biochem. Biophys. Res. Commun. 182:1246-1253(1992).
CC	-1 MISCELLANEOUS: THIS PROTEIN BINDS TWO CALCIUM IONS.
CC	-1 SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND
CC	MORE SPECIFICALLY TO S-100/CABP LINE PROTEINS.
CC	-----
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CC	-----
DR	EMBL; X65614; CAA65614.1; -.
DR	PIR; S24146; S24146.
DR	HSP; P02638; ICFP.
DR	MIM; 600614; -.
DR	PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR	PROSITE; PS00303; S100_CABP; 1.
DR	Pfam; PF00036; ehand; 1.
DR	Pfam; PF01023; S_100; 1.
KW	Calcium-binding; Placenta.
FT	CA_BIND 19 32 SITE 1 (LOW AFFINITY).
FT	CA_BIND 62 73 SITE II (HIGH AFFINITY).
FT	CONFLICT 32 32 E -> T (IN REF. 2).
FT	CONFLICT 44 44 F -> E (IN REF. 2).
SQ	SEQUENCE 95 AA; 10400 MW; EAAC214C CRC32;

```

Query Match      33.6%; Score 87; DB 1; Length 95;
Best Local Similarity 46.0%; Pred. No. 0.00015;
Matches 23; Conservative 7; Mismatches 20; Indels 0; Gaps

OY      1 TKLEDELEGIIINGHOYSVRVGHFTLTKRYELKQGLTKEPLPTXONXKDQ 50
          I::I:: :::: :::: | ||| |||| |::|:: ||:
Db       2 TELETAGMTIDVFSSRGSESGSTQLTRGSELKVLMEKELPGLQSGHDK 51

RESULT 12
SI04_RAT SI04_RAT STANDARD; PRT; 101 AA.
AC P05942;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PLACENTAL CALCIUM-BINDING PROTEIN (NERVE GROWTH FACTOR INDUCED PROTEIN
DE 42A) (P9K).
GN S100A4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RA SEQUENCE FROM N.A.
RX MEDLINE; 88125019.
RX MASIAKOWSKI P., SHOOTER E.M.;
RT "Nerve growth factor induces the genes for two proteins related to a
RT family of calcium-binding proteins in PC12 cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1277-1281(1988).
RN [2]
RA SEQUENCE FROM N.A.
RX MEDLINE; 88118907.
RX BARRACLOUGH R., SAVIN J., DUBE S.K., RUDLAND P.S.;
RT "Molecular cloning and sequence of the gene for p9Ka, A cultured
RT myoepithelial cell protein with strong homology to S-100, a calcium-
RT binding protein.";
RL J. Mol. Biol. 198:13-20(1987).
RN [3]
RA SEQUENCE OF 3-101 FROM N.A.
RX STRAIN-OSBORNE-MENDEL; TISSUE-KIDNEY;
RX MEDLINE; 92158347.
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RA BAUDIER J GLASSER N., HAGLID K, GERARD D.;  

RT "Purification, characterization and ion binding properties of human  

RL brain S100b protein.";  

RL Biochim. Biophys. Acta 790:164-173(1984).  

RN [4]  

RP STRUCTURE BY NMR.  

RX MEDLINE: 98179937.  

RA SMITH S.P., SHAW G.S.;  

RT "A novel calcium-sensitive switch revealed by the structure of human  

RL S100b in the calcium-bound form.";  

RL Structure 6:211-222(1998).  

CC -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY-  

CC DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH  

CC IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM  

CC ION ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY  

CC AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.  

CC -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR  

CC ONE ALPHA AND ONE BETA CHAIN.  

CC -1- SUBCELLULAR LOCATION: CYTOSOLASMIC.  

CC -1- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE  

CC BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES.  

CC -1- MISCELLANEOUS: IN ADDITION TO METAL-ION BINDING, THIS PROTEIN IS  

CC INVOLVED WITH THE REGULATION OF PROTEIN PHOSPHORYLATION IN BRAIN  

CC TISSUE.  

CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND  

CC MORE SPECIFICALLY TO S-100/CABP LIKE PROTEINS.  

CC -----  

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CC -----  

DR EMBL: M59488; AAA60367.1; -  

DR EMBL: M59487; AAA60367.1; JOINED.  

DR PIR: A03076; BCHUIB.  

DR PIR: A38364; A38364.  

DR PDB: 1UMO; 10-JUN-98.  

DR MIM: 176890; -  

DR PROSITE; PS00018; EF_HAND. 1.  

DR PROSITE; PS00303; S100_CABP; 1.  

DR PIR: PF00036; efhand; 1.  

DR PIR: PF01023; S_100; 1.  

KW Calcium-binding; Zinc; Metal-binding; 3D-structure.  

FT INIT_MET 0  

FT MOD_RES 1  

FT CA_BIND 18 31 SITE 1 (LOW AFFINITY).  

FT CA_BIND 61 72 SITE II (HIGH AFFINITY).  

SQ SEQUENCE 91 AA; 10582 MW; 790FF3B9 CRC32;  

  

QY 1 TKLDHLEGIINIGHOYSVRVGHFDTLNKKYELKQGTKEPKTLQNXMDQ 50  

DB 1 SELERKAWALIDVPHOYSGREGDKHKRKSELKELINNELSHFLEIRKQ 50  

  

RESULTS 14  

S10B_MOUSE STANDARD; PRT; 91 AA.  

AC PS0114;  

DT 01-OCT-1996 (Rel. 34, Created)  

DT 01-OCT-1996 (Rel. 34, Last sequence update)  

DT 01-OCT-1996 (Rel. 34, Last annotation update)  

DE S-100 PROTEIN, BETA CHAIN.  

DE S100B.  

OS Mus musculus (Mouse).  

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

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RESULT      1
0933395
ID          093395      PRELIMINARY;      PRN:      101 AA.
AC          093395;
DT          01-NOV-1998 (TrEMBLrel. 08, Created)
DT          01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT          01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE          S100-LIKE CALCIUM BINDING PROTEIN.
GN          S100.
OS          Salvelinus fontinalis (Brook trout).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Actinopterygii;
OC          Neopterygii; Teleostei; Euteleostei; Protacanthopterygii;
OC          Salmoniformes; Salmonidae; Salvelinus.
RN          [1]
RP          SEQUENCE FROM N.A.
RC          TISSUE-OVULATORY OVARY;
RA          BOBE J.M., GOETZ F.W.;
RT          "Downregulation of a S100-like calcium binding protein in the brook
RL          trout ovary following ovulation.";
RN          [2]
RP          Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
RC          TISSUE-OVULATORY OVARY;
RA          LANGENAU D.M., GOETZ F.W.;
RL          Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR          EMBL: AF077613; AAC28367.1; -.
DR          HSSP: P02633; IBOC.
DR          PROSITE: PS00303; S100_CABP; 1.
DR          PFMAM: PF00036; ehand; 1.
DR          PFMAM: PF01023; S_100; 1.
SQ          SEQUENCE      101 AA;      11285 MW;      DDBFC2E8 CRC32;

Query Match      34.7%;      Score 90;      DB 13;      Length 101;
Best Local Similarity      38.8%;      Pred. No. 0.0008;
Matches      19;      Conservative      13;      Mismatches      17;      Indels      0;      Gaps      0;

1      TKLEDHLEGINIGHQSVRYGHFDITLNKYLKQLGTGLKELPKTLONKQD      49
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
3      SQLESMSMLTTFVHRVYADKDGDCNTLSKRLKELMQLMQLTSLASFLKSQD      51

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001720
ID 001720 PRELIMINARY; PRT; 591 AA.
AC 001720;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE FILAGRIN PRECURSOR (PROFILAGRIN) (FRAGMENT).
GN F4G.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-PLACENTA;
RX MEDLINE: 93054736.
RA PRESLAND R.B., HAYDOCK P.V., FLECKMAN P., NIRUNSUJIRI W., DALE B.A.;
RT "Characterization of the human epidermal profilaggrin gene. Genomic
RT organization and identification of an S-100-like calcium binding
RT domain at the amino terminus."
RL J. Biol. Chem. 267:23772-23781(1992).
-1- FUNCTION: AGGREGATES KERATIN INTERMEDIATE FILAMENTS AND PROMOTES
DISULFID-BOND FORMATION AMONGST THE INTERMEDIATE FILAMENTS DURING
TERMINAL DIFFERENTIATION OF MAMMALIAN EPIDERMIS.
-1- PTM: FILAGRIN IS INITIALLY SYNTHESIZED AS A LARGE, INSOLUBLE,
HIGHLY PHOSPHORYLATED PRECURSOR CONTAINING MANY TANDEM COPIES OF
324 AA. THE PRECURSOR IS DEPOSITED AS KERATOHYALIN GRANULES.
CC DURING TERMINAL DIFFERENTIATION IT IS DEPHOSPHORYLATED &
PROTEOLYTICALLY CLEAVED.
CC POLYMORPHISM: A NUMBER OF PROFILAGRIN ISOFORMS HAVE BEEN FOUND
WHICH DIFFER BOTH IN SEQUENCE AND IN THE NUMBER OF FILAGRIN
REPEATS.
CC EMBL: L01089; AAA60177.1; -.
DR EMBL: L01090; AAA60176.1; -.
DR HSSP: P30801; ICNP.
DR MIM: 135940; -.
DR PRAM: PR00036; efband. 1.
DR PRAM: PF01023; S_100; 1.
KW Polymorphism.
FT PROPEP 1 293 POTENTIAL.
FT CHAIN 294 467 FILAGRIN.
FT PROPEP 468 474 POTENTIAL.
FT CHAIN 475 >591 FILAGRIN.
FT CA_BIND 19 32 SITE I (BY SIMILARITY).
FT NON_TER 62 73 SITE II (BY SIMILARITY).
SQ SEQUENCE 591 AA; 66366 MW; 747C0F83 CRC32;

Query Match 31.3%; Score 81; DB 4; Length 591;
Best Local Similarity 42.6%; Pred. No. 0.066;
Matches 20; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

OY 3 LEDHLEGIINIGHQYSVRGHFDLTKYELKGLTKELPKTLQXKD 49
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 4 LLENIFALINLFKQYSKKDKNTDLSKKELEKEFRQILKNPDD 50

RESULT 3
ID 005331 PRELIMINARY; PRT; 1218 AA.
AC 005331;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE FILAGRIN (PROFILAGRIN) (FRAGMENT).
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-FORESKIN;
RX MEDLINE: 93109348.
RA MARKOVA N.G., MAKEKOV L.N., CHIRIEV C.C., GAN S.-O., IDLER W.W.,

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RA STEINERT P.M.;
RT "Profilaggrin is a major epidermal calcium-binding protein."
RL Mol. Cell. Biol. 13:613-625(1993).
-1- FUNCTION: AGGREGATES KERATIN INTERMEDIATE FILAMENTS AND PROMOTES
DISULFID-BOND FORMATION AMONGST THE INTERMEDIATE FILAMENTS DURING
TERMINAL DIFFERENTIATION OF MAMMALIAN EPIDERMIS.
-1- PTM: FILAGRIN IS INITIALLY SYNTHESIZED AS A LARGE, INSOLUBLE,
HIGHLY PHOSPHORYLATED PRECURSOR CONTAINING MANY TANDEM COPIES OF
324 AA. THE PRECURSOR IS DEPOSITED AS KERATOHYALIN GRANULES.
CC DURING TERMINAL DIFFERENTIATION IT IS DEPHOSPHORYLATED &
PROTEOLYTICALLY CLEAVED.
CC POLYMORPHISM: A NUMBER OF PROFILAGRIN ISOFORMS HAVE BEEN FOUND
WHICH DIFFER BOTH IN SEQUENCE AND IN THE NUMBER OF FILAGRIN
REPEATS.
CC EMBL: M96943; AAA36487.1; -.
DR HSSP: P30801; ICNP.
DR PRAM: PR00036; efband. 1.
DR PRAM: PF01023; S_100; 1.
KW Phosphorylation; Polyprotein; Developmental protein; Calcium-binding;
KW Polymorphism.
FT CA_BIND 19 32 SITE I (BY SIMILARITY).
FT NON_TER 62 73 SITE II (BY SIMILARITY).
SQ SEQUENCE 1218 AA; 133605 MW; F52F278C CRC32;

Query Match 29.7%; Score 77; DB 4; Length 1218;
Best Local Similarity 45.0%; Pred. No. 0.43;
Matches 18; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

OY 10 IINIGHQYSVRGHFDLTKYELKGLTKELPKTLQXKD 49
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 11 IINLFNEYSKKDKNTDLSKKELEKEFRQILKNPDD 50

RESULT 4
ID 09YH57 PRELIMINARY; PRT; 217 AA.
AC 09YH57;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE P26OLF.
GN P26OLF CDNA.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-OLFACTORY;
RX MEDLINE: 99008915.
RA MIWA N., KOBAYASHI M., TAKAMATSU K., KAWAMURA S.;
RT "Purification and molecular cloning of a novel calcium-binding
RT protein, p26OLF, in the frog olfactory epithelium."
RL Biochem. Biophys. Res. Commun. 251:860-867(1998).
DR EMBL: D50333; BAA34388.1; -.
DR HSSP: P08206; 1BT6.
SQ SEQUENCE 217 AA; 24494 MW; 90FB7718 CRC32;

Query Match 25.1%; Score 65; DB 13; Length 217;
Best Local Similarity 30.6%; Pred. No. 1.8;
Matches 15; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

OY 1 TKLEHLEGIINIGHQYSVRGHFDLTKYELKGLTKELPKTLQXKD 49
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 10 TEMERSERKILITVFORAGKEGNTTSNFKERFQFMAALGSEFTKXKD 58

RESULT 5
ID 09X1L8 PRELIMINARY; PRT; 438 AA.
AC 09X1L8;

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DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE FIX PROTEIN.
 GN TMA32.
 OS Thermotoga maritima.
 SC Bacteria; Thermotogales; Thermotoga.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 99287316.
 RA NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
 RA HART D.H., HICKY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
 RA McDONALD L., UTTERBACK T.R., MALEK J.A., LINNER K.D., GARRETT M.M.,
 RA STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
 RA HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
 RA SMITH H.O., VENTER J.C., FRASER C.M.;
 RT "Evidence for lateral gene transfer between Archaea and bacteria from
 genome sequence of *Thermotoga maritima*."
 RT Nature 399:323-329(1999).
 [2]
 SEQUENCE FROM N.A.
 RA NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
 RA HART D.H., HICKY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
 RA McDONALD L., UTTERBACK T.R., MALEK J.A., LINNER K.D., GARRETT M.M.,
 RA STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
 RA HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
 RA SMITH H.O., VENTER J.C., FRASER C.M.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A6001800; AAC36599.1; -
 SO SEQUENCE 438 AA; 48974 MW; F8E8008A CRC32;

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Query Match      23.4%: Score 60.5; DB 2; Length 438;
Best Local Similarity 29.3%: Pred. No. 13;
Matches 17; Conservative 11; Mismatches 15; Infields 15; Gaps 2

QY      8 EGINIGHQ-----YSVRGHFDPLNKLKQLGTKEKLPK-----LQNXKDQ 50
          :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db      86 EGVIGHHNVNWKENPNNAFTVLRADFEDWMEQOEYKAGALLIPKRVVEDELFNNGE 143

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RESULT	6		
P79342		PRELIMINARY;	PRT; 98 AA.
AC	P79342;		
DT	01-MAY-1997 (TREMBLrel. 03, Created)		
PT	01-MAY-1997 (TREMBLrel. 03, last sequence update)		
	01-NOV-1999 (TREMBLrel. 12, last annotation update)		
	8kDa AMLEXANOX-BINDING PROTEIN.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Mammalia;		
	Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;		
OC	Bovine; Bos.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	OTAMA Y., SHISHIBORI T., MATSUTOMO M., YAMASHITA K., MAETA H.,		
RA	KOBAYASHI R.;		
RT	"Molecular cloning of a new 8kDa protein, isolated with Amlexanox		
RT	couple d column chromatography."		
RL	Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; AB001567; BAA19411.1; -		
DR	HSSP; P30801; ICNP.		
DR	PRAM; PF01023; S_100; 1.		
SO	SEQUENCE, 98 AA; 11233 MW; 70331499 CRC32;		

Query Match	23.2%	Score 60:	DB 6:	length 98:
Best Local Similarity	30.4%	Pred. No. 3:		
Matches	14:	Conservative	13:	Mismatches 19:
				Indels 0:
				Gaps 0

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RESULT      7
09ZIB5
ID          09ZIB5      PRELIMINARY;      PRT: 1238 AA.
AC          09ZIB5.
DT          01-MAY-1999 (TREMBLrel. 10, Created)
DT          01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT          01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE          S-LAYER-RTX PROTEIN.
GN          CSXB.
OS          Wolinella recta.
OC          Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
CC          Campylobacter.
RN          [1]
RP          SEQUENCE FROM N.A.
RC          STRAIN-ATCC33238;
RA          BRAUN M., FREY J., KUHNER P.;
RT          "Characterization of antigenic bistructural S-layer-RTX proteins from
RT          Campylobacter rectus."
RL          Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR          EMBL; AF035192; AAD02003.1; -.
DR          PROSITE; PS00330; HEMOLYSIN_CACDUM; 11.
SQ          SEQUENCE 1238 AA; 130821 MW; F868B05C CRC32;

Query Match      22.6%; Score 58.5; DB 2; Length 1238;
Best Local Similarity 26.7%; Pred. NO. 73;
Matches 16; Conservative 10; Mismatches 23; Indels 11; Gaps 1;

Cy      2 KLEDDLEGIINIG-----HQYSVRGVGHPTLTKKYLELKOIGTKELPKTLQNXKQD 50
Db      606 KIEGDLKIILIDGGEGVDTLAEDHEIDNALQAMINKFETLIDGSGNNPKTLRLATPQ 665

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RESULT	8			
050262				
ID	050262	PRELIMINARY;	PTI;	193 AA.
AC	050262;			
DT	01-NOV-1996	(TEMBUREl. 01, Created)		
DT	01-NOV-1996	(TEMBUREl. 01, last sequence update)		
DT	01-AUG-1998	(TEMBUREl. 07, last annotation update)		
DE	APPLE PROLIFERATION, STRAIN AT NITROREDUCTASE LIKE PROTEIN			
DE	(FRAGMENT).			
OS	Phytoplasma. sp.			
OC	Bacteriia: Firmicutes: Bacillus/Clostridium group; Mollificutes			
OC	Acidoleplasmataceae; Phytoplasma.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-APPLE PROLIFERATION, STRAIN AT;			
RA	SAILLARD C., JARAUSCH W., DOSBA F., BOVE J.;			
RL	submitted (Apr-1994) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: L22217; AAA18507.1; -			
FT	NON_TER	193	193	
EQ	SEQUENCE	193 AA;	22105 MM;	5030498C CRC32;

Query Match	21.6%	Score 56;	DB 2;	Length 193;
Best Local Similarity	30.0%	Pred. NO. 19;		
Matches 12; Conservative	11; Mismatches	15; Indels	2; Gaps	1;
Oy	10	IINIGHOSVVRGHFDLTINKYELKGTGTEPKTQONXKD	49	
		: : :: :: :: :		
Db	133	IIVDRNHYEYOLGFHKNAINPKINF--RELPLEWENKNK	170	
RESULT	9			
Q92458				
ID	Q92458	PRELIMINARY;	PRT:	797 AA.
AC	Q92458;			
DT	01-FEB-1997	(TREMBLrel. 02; Created)		
DT	01-JUN-1998	(TREMBLrel. 06; Last sequence update)		
DT	01-MAY-1999	(TREMBLrel. 10; Last annotation update)		


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DE (FATTY ACID DESATURASE 1).
GN OLE1.
OS Mucor rouxii.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC Mucor.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 24905;
RA LAOTENG K., ANJARD C., CHEEVADHANARAK S., TANTICHAROEN M.,
RA RACHADAMONG S.;
RU Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: STEAROYL-COA + AH(2) + O(2) -> CLEOYL-COA + A +
CC 2 H(2)O.
CC -1- COFACTOR: IRON.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
DR EMBL: AF026401; AAB82294.1; -.
DR HSSP: P00173; 1IEU.
DR PROSITE: PS00476; FATTY_ACID_DESATUR_1; 1.
DR PFAM: PF01069; Desaturase; 1.
DR PRINTS: PR00075; FACDSATRASE.
KW Oxidoreductase; Fatty acid biosynthesis; Iron; Membrane;
KW Endoplasmic reticulum.
SQ SEQUENCE 452 AA; 51963 MW; B8FE5F48 CRC32;

Query Match 21.0%; Score 54.5; DB 3; Length 452;
Best Local Similarity 28.8%; Pred. No. 73;
Matches 15; Conservative 6; Mismatches 14; Indels 17; Gaps 2;

QY 8 EGIINIGHQY-----SVRVGHEDTLN-----KYLKQLGTRELPK 42
DB 263 EGYHNFHNPQPDYRNAIKFGQYDPTKMKIIVLSWFGIAYELKQFPNNEYVK 314

RESULT 14
O49356 PRELIMINARY; PRT; 444 AA.
ID O49356
AC O49356;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DE 01-JUN-1998 (TEMBLrel. 06, Last annotation update)
DE FERREDOXIN-NADP+ REDUCTASE - LIKE PROTEIN.
GN F10M6.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RA BEVAN M., WEICHELSEKARTNER M., FARTMANN B., GRANDERATH K., DAUNER D.,
RA HERZL A., NEUMANN S., HOEHLSEL J., MEWES H.W., MAYER K., SCHUELLER C.;
RU Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL021811; CAA16955.1; -.
SQ SEQUENCE 444 AA; 48698 MW; 3F3BB4A2 CRC32;

Query Match 20.8%; Score 54; DB 10; Length 444;
Best Local Similarity 30.4%; Pred. No. 82;
Matches 14; Conservative 7; Mismatches 15; Indels 10; Gaps 2;

QY 6 HLEGI-----INGHOYSVRVGHEDTLN-KYLKQLGTRELP 41
DB 267 HVSQVNLQKTLTISVGTGQIAVGTGEFEDLNCMVLAIGKSP 312

RESULT 15
O04053 PRELIMINARY; PRT; 625 AA.
ID O04053
AC O04053;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)

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DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE D9461.13P.
GN D9461.13.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RA DIETRICH F.S.;
RU Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA DIETRICH F.S., MULLIGAN J., ALLEN E., ARAUJO R., AVILES E., BERNO A.,
RA CARPENTER J., CHEN E., CHERRY J.M., CHUNG E., DUNCAN M.,
RA HUNICKER-SMITH S., HYMAN R., KOMP C., LASHKARI D., LEW H., LIN D.,
RA MOSEDALE D., NAKAHARA K., NAMATH A., OEFNER P., OH C., PETEL F.X.,
RA ROBERTS D., SCHRAMM S., SCHROEDER M., SHOKREN T., SHROFF N.,
RA WINANT A., YELTON M., BOTSTEIN D., DAVIS R.W.;
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RN [3]
RP SEQUENCE FROM N.A.
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DR EMBL: U33007; AAB64858.1; -.
DR PFAM: PF00787; PX; 1.
DR SEQUENCE 625 AA; 70740 MW; 29A8257F CRC32;

Query Match 20.8%; Score 54; DB 3; Length 625;
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 8; Mismatches 10; Indels 10; Gaps 2;

QY 14 GHQYSVRVG---HFDT-----LNKYLKQLGTRELPKTLQ 45
DB 509 GHQNEIHIGASKLNKTKSTPTMNLKLEIKQLTQERSKQIK 550

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Search completed: March 14, 2000, 15:47:29
 Job time: 623 sec

